

GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds  
(without alignments)  
46.851 Million cell updates/sec

## Title: US-10-062-257A-1

## Perfect score: 45

## Sequence: 1 TFDYLRSQL 9

## Scoring table: BL0SUM62

## Gapop 10.0 , Gapext 0.5

## Searched: 2589679 seqs, 457216429 residues

## Total number of hits satisfying chosen parameters: 2589679

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Database : A\_Geneseq\_8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	AAG68079	Aag68079 Antitumou
2	45	100.0	9	AAB73117	Aab73117 Tumour an
3	45	100.0	9	ABR84376	Abr84376 Human lck
4	45	100.0	9	ADS87117	Ad887117 Human gen
5	45	100.0	9	ADX58317	Adx58317 Partial a
6	45	100.0	9	ADZ42232	Adz42232 Cytotoxic
7	45	100.0	9	AEC33132	Aec33132 Lck tumor
8	45	100.0	13	AAB73144	Aab73144 Tumour an
9	45	100.0	246	ABG2263	Abg2263 Novel hum
10	45	100.0	259	AAY43956	Aay43956 Mouse pro
11	45	100.0	259	AAY43955	Aay43955 Human pro
12	45	100.0	263	ADR88385	Adr88385 LCK tyros
13	45	100.0	265	ABR56203	Abrr56203 Mutant Ly
14	45	100.0	271	ABR56204	Abrr56204 Mutant Ly
15	45	100.0	279	ADY85449	Ady85449 Catalytic
16	45	100.0	346	AAE06208	Aae06208 Human pro
17	45	100.0	346	ABB84435	Abb84435 Human pro
18	45	100.0	346	ABM82980	Abm82980 Human dia
19	45	100.0	355	ABM82980	Abm82980 Human dia
20	45	100.0	417	AAR14201	Aar14201 (Beta-gal
21	45	100.0	458	ADC99048	Adc99048 Human kPP
22	45	100.0	502	AAE21689	Aae21689 Fugu rubr
23	45	100.0	508	AAB37700	Aab37700 Human lym

24	45	100.0	508	7	ADE58802 Human Pro
25	45	100.0	508	7	Ade58799 Human Pro
26	45	100.0	508	7	Adf45072 Human kin
27	45	100.0	508	7	Adl34479 Human lym
28	45	100.0	508	8	Ads88148 Human pro
29	45	100.0	509	3	Aay49420 PKA subst
30	45	100.0	509	6	Abr58699 Human can
31	45	100.0	509	7	Abr56202 Human lym
32	45	100.0	509	7	Ade40449 Human pro
33	45	100.0	509	8	Adl22907 Human MP2
34	45	100.0	509	8	Adp12458 Protein e
35	45	100.0	509	8	Adp48374 Human lym
36	45	100.0	509	9	Adz51107 Amino aci
37	45	100.0	509	9	Aea35921 Human lck
38	45	100.0	539	8	Abm82981 Human dia
39	45	100.0	539	8	Abm82982 Human dia
40	45	100.0	551	4	Abg22264 Novel hum
41	45	100.0	567	5	Abg79673 Tumour in
42	41	91.1	9	4	Aab73123 Tumour an
43	41	91.1	13	4	AAB73149 Tumour an
44	41	91.1	251	2	ADY43954 Human tra
45	41	91.1	439	9	ADY52633 Human tra
46	41	91.1	447	9	ADY52633 Human tra
47	41	91.1	452	9	ADY52633 Human tra
48	41	91.1	459	9	ADY52631 Human tra
49	41	91.1	467	9	ADY52630 Human tra
50	41	91.1	472	9	ADY52629 Human tra
51	41	91.1	473	9	ADY52628 Human tra
52	41	91.1	481	9	ADY52627 Human tra
53	41	91.1	483	9	ADY52626 Human tra
54	41	91.1	493	9	ADY52625 Human tra
55	41	91.1	511	7	ADF45073 Human kin
56	41	91.1	512	7	Add19014 Human dis
57	41	91.1	512	7	Adn95430 Human BBC
58	41	91.1	512	8	Adl22908 Human MP2
59	41	91.1	512	8	Adn0498 Antipsori
60	41	91.1	512	8	Adr142483 Protein e
61	41	91.1	512	8	Adp12483 PRO polyp
62	41	91.1	512	8	Adp23372 PRO polyp
63	41	91.1	512	8	Ady16487 PRO polyp
64	41	91.1	512	9	Ady19685 PRO polyp
65	41	91.1	512	8	Ady14848 PRO polyp
66	41	91.1	512	8	Ady52574 Human onc
67	41	91.1	512	8	Aea35920 Human lym
68	41	91.1	512	9	Adh22508 Human tra
69	41	91.1	512	9	Abm84024 Human dia
70	41	91.1	512	8	Adu24099 Human asp
71	41	91.1	512	9	Abp52121 Homo sapi
72	37	82.2	559	8	Adel10036 Novel pro
73	37	82.2	561	8	Aaw14055 Pumpkin e
74	37	82.2	561	5	Adm98975 Diterpene
75	37	82.2	606	5	Ade08716 Novel pro
76	37	82.2	620	7	Aay29671 Human src
77	37	82.2	789	2	Aau08733 Src-famil
78	37	82.2	789	8	Abu27400 Protein e
79	37	82.2	822	7	Ade08716 Novel pro
80	36	80.0	260	2	Aay29668 Human src
81	36	80.0	308	6	Aab73144 Tumour an
82	36	80.0	308	6	Abg2263 Novel hum
83	36	80.0	319	2	Aay37655 Amino aci
84	36	80.0	496	2	Aay29668 Human src
85	36	80.0	496	4	Aab08734 Xenopus 1
86	36	80.0	496	4	Aau08730 Xenopus 1
87	36	80.0	496	4	Aau08735 Xenopus 1
88	35	77.8	9	Aab73124 Tumour an	
89	35	77.8	13	4	Aay6750 Antitumou
90	35	77.8	13	4	Aab08730 Tumour an
91	35	77.8	250	9	Ady52570 Human onc
92	35	77.8	259	2	Aay43957 Human pro
93	35	77.8	271	8	ADR88384 HCK tyros
94	35	77.8	272	5	ABB81188 Human KIT
95	35	77.8	300	9	Ady85468 Catalytic
96	35	77.8	316	9	Ady85448 Catalytic

100	97	35	77.8	383	7	ADJ68978
99	98	35	77.8	436	8	ADN61468
99	98	35	77.8	438	9	ADY52642
35	77.8	458				ADJ71657

## ALIGNMENTS

Adj68978	Human	hea	AC	AAB73117;
Adn61468	Human	KPP	XX	
Ady52642	Human	tra	DT	09-MAY-2001 (first entry)
Adj71657	Human	NOV	XX	

tumour antigen peptide #1.  
src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.  
*Homo sapiens.*

AAG68079  
ID AAG68079 standard; peptide; 9 AA.

AA  
AC  
XX  
AAG68079;

BT  
xx  
xx  
17-DEC-2001 (first entry)

XX  
KW  
Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;

**KW** tumour specific cytotoxic T lymphocyte; anticancer; SAR1-1; SAR1-3;  
**KW** cyclophilin B gene; HLA-A2402.

OS  
XX  
Homo sapiens.

11-SEP-2001 11:22:59,2 n.  
XX  
PD

XX  
PP  
YY  
25-DEC-2000; 2000JP-00393047.

PR 28-DEC-1999; 99JP-00374322.  
XX

FA  
XX  
DR  
WPI: 2001-610076/70:  
(1101) / 110 1:

PT  
XX  
New peptides for recognizing cancer cells with tumor specific cytotoxi

XX  
PS Claim 8; Page 2; 14pp; Japanese.

xx  
cc  
cc  
The present invention describes peptides recognising cancer cells with  
tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising

CC cancer cells with tumour specific CTLs are selected from: (1) peptides sequences (AAG68066 to AAG68069); (2) peptides containing the above

the above mentioned sequences; and (4) peptides with one or more deleted, added or inserted amino acid(s) of the above mentioned

CC sequences, particularly those having recognising property due to HLA-CC A2402 binding CTL, especially having at least 5 amino acids, used for CC medicine particularly anticancer agents derived from antitumour

CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B genes. The antitumour peptides have cytostatic activities. The peptide

XX  
SQ Sequence 9 AA;

Query Match Score 45; DB 4; Length 9;  
Best Local Similarity Pred. No. 2.1e+06;

OV 1 TEDYIERSV!; 9 Matches 9; Conservative 0; Mismatches 0; Indels 0; gaps

Db  
1 TFDYLRSVL 9

RESULT 2  
AAB73117  
ID AAB73117 standard; peptide; 9 AA.  
XX

AC AAB73117;  
 XX DT 09-MAY-2001 (first entry)  
 XX DE Tumour antigen peptide #1.  
 XX KW Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.  
 XX OS Homo sapiens.  
 XX PN WO200111044-A1.  
 XX PD 15-FEB-2001.  
 XX PF 03-AUG-2000; 2000WO-JP005220.  
 XX PR 05-AUG-1999; 99JP-00222101.  
 XX PA (ITOH/) ITOH K.  
 XX PI Itoh K;  
 XX DR WPI; 2001-191541/19.  
 XX PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and  
 PT polynucleotides encoding them for treatment of cancer.  
 XX PS Claim 1; Page 66; 75pp; Japanese.  
 XX CC The present invention relates to peptides which are partial sequences of  
 CC src/lck family proteins. The present sequence is one such peptide. The  
 CC peptides are useful for producing vaccines for the treatment of cancer,  
 CC including colon cancer and small-cell lung cancer  
 XX SQ Sequence 9 AA;  
 RESULT 3  
 ABR84376  
 ID ABR84376 standard; peptide; 9 AA.  
 XX AC ABR84376;  
 XX DT 06-NOV-2003 (first entry)  
 DE Human lck HLA-A24 epitope, SEQ ID NO:26.  
 XX Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;  
 KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;  
 KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;  
 KW human; human leukocyte antigen; HLA-A24 epitope.  
 XX OS Homo sapiens.  
 XX PN JP2002365286-A.  
 XX PD 18-DEC-2002.  
 XX PF 18-SEP-2001; 2001JP-00283413.  
 XX PR 13-NOV-2000; 2000JP-00345094.  
 XX PA (ITOY/) ITO Y.  
 DR WPI: 2003-508315/48.

XX  
XX A detection method of antigen specific T-cells, comprises the use of  
PT plural antigenic peptides, useful in semi-quantitative determination of  
PT cancer specific T-cell frequencies and for monitoring cellular immunity.  
XX

PS Example 8; Page 10; 18pp; Japanese.

XX  
CC The invention relates to a method for the detection of antigen specific T  
CC -cells in a blood sample involving the use of a plurality of antigenic  
peptides. The method comprises sampling of peripheral blood monocytes;  
CC stimulation of the collected peripheral blood monocytes with antigens  
without direct use of antigen presenting cells; and detection of T-cells  
specific to the antigen in the stimulated monocytes. The method is  
particularly used for the detection of cancer as it can be used in semi-  
quantitative determination of cancer specific T-cells. It can also be  
used for cancer vaccine therapy for patients with cervical or prostate  
cancer. The method can additionally be used to monitor of cellular  
immunity and cancer immune therapy by detection of specific T-cell  
frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human  
leukocyte antigen) peptides of human origin used in an example from the  
invention

XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
Db 1 TFDYLRSQL 9

RESULT 4  
ADS87117

ID ADS87117 standard; peptide; 9 AA.

XX  
XX AC ADS87117;

XX DT 21-APR-2005 (first entry)

XX DE Partial antigenic peptide #3 derived from p56.

XX KW cytostatic; vaccine; hematopoietic tumor; p56; immunotherapy.

XX OS Unidentified.

XX PN WO2005011723-A1.

XX PD 10-FEB-2005.

XX PF 05-AUG-2004; 2004WO-JP011232.

XX PR 05-AUG-2003; 2003JP-00287208.

XX PA (ITOH) ITOH K.

XX PI Itoh K;

XX DR WPI; 2005-152358/16.

XX Prevention and/or therapeutic agent of hematopoietic tumor useful for  
PT preventing and/or treating hematopoietic tumor, has peptides having amino  
PT acid sequences of partial peptide of p56lck, SART-1, SART-2, SART-3, or  
PT ART-1 protein.

XX PS Claim 1; SEQ ID NO 3; 41pp; Japanese.

XX CC The specification describes a remedy for a hematopoietic tumor. The  
CC remedy comprises one or more peptides derived from p56 (lck), SART-1,  
CC SART-2, SART-3, or ART-1 proteins as an active ingredient. The peptides  
XX induce specific cytotoxic T cells. The remedy of the invention is useful  
PR for preventing and treating hematopoietic tumors comprising human  
leukocyte antigen (HLA)-A24 molecules on its cell surface. It is also  
PA (KYUS-) KYUSHU TLO CO LTD.  
XX useful in immunotherapy of hematopoietic tumors, and for treating  
PI malignant tumors such as acute myelogenous leukemia, acute lymphoblastic  
XX leukemia, chronic lymphocytic leukemia, malignant lymphoma, multiple  
WPI; 2004-357144/33.  
XX myeloma, etc. The present sequence represents a partial peptide derived  
PT from p56, and is used in the remedy of the invention.

XX PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes  
PT or cytokine genes for prevention and treatment of cancer.

XX PS Disclosure; SEQ ID NO 133; 266pp; Japanese.

CC The invention relates to a novel genetic vaccine containing the ubiquitin  
gene together with a gene encoding an antigenic protein containing a T-  
cell target sequence. The vaccine of the invention may be useful for  
CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma  
CC

CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer  
CC of the lung, stomach, skin, ovary, prostate, womb, pancreas,  
CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence  
CC is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide  
CC of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 45; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.1e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
Db 1 TFDYLRSQL 9

RESULT 5  
ADX58317

ID ADX58317 standard; peptide; 9 AA.

XX AC ADX58317;

XX DT 21-APR-2005 (first entry)

XX DE Partial antigenic peptide #3 derived from p56.

XX KW cytostatic; vaccine; hematopoietic tumor; p56; immunotherapy.

XX OS Unidentified.

XX PN WO2005011723-A1.

XX PD 10-FEB-2005.

XX PF 05-AUG-2004; 2004WO-JP011232.

XX PR 05-AUG-2003; 2003JP-00287208.

XX PA (ITOH) ITOH K.

XX PI Itoh K;

XX DR WPI; 2005-152358/16.

XX Prevention and/or therapeutic agent of hematopoietic tumor useful for  
PT preventing and/or treating hematopoietic tumor, has peptides having amino  
PT acid sequences of partial peptide of p56lck, SART-1, SART-2, SART-3, or  
PT ART-1 protein.

XX PS Claim 1; SEQ ID NO 3; 41pp; Japanese.

XX CC The specification describes a remedy for a hematopoietic tumor. The  
CC remedy comprises one or more peptides derived from p56 (lck), SART-1,  
CC SART-2, SART-3, or ART-1 proteins as an active ingredient. The peptides  
XX induce specific cytotoxic T cells. The remedy of the invention is useful  
PR for preventing and treating hematopoietic tumors comprising human  
leukocyte antigen (HLA)-A24 molecules on its cell surface. It is also  
PA (KYUS-) KYUSHU TLO CO LTD.  
XX useful in immunotherapy of hematopoietic tumors, and for treating  
PI malignant tumors such as acute myelogenous leukemia, acute lymphoblastic  
XX leukemia, chronic lymphocytic leukemia, malignant lymphoma, multiple  
WPI; 2004-357144/33.  
XX myeloma, etc. The present sequence represents a partial peptide derived  
PT from p56, and is used in the remedy of the invention.

XX PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes

XX or cytokine genes for prevention and treatment of cancer.





CC interaction of a protein with other molecules  
 XX Sequence 259 AA;  
 SQ Query Match 100.0%; Score 45; DB 2; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 0.91; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSQL 9  
 244 TFDYLRSQL 252

Db

RESULT 11  
 AAY43955  
 ID AAY43955 standard; protein; 259 AA..  
 XX AC  
 XX AAY43955;  
 DT 21-DEC-1999 (first entry)  
 XX DE Human protein kinase #15.  
 KW Prediction; secondary structure; alignment; evolutionary conservation; homology; periodicity; co-variation analysis; antigenic site; site directed mutagenesis; interaction.  
 KW OS Homo sapiens.  
 XX OS  
 PN US5958784-A.  
 XX PN 02-SEP-2004.  
 XX PD 28-FEB-2003; 2003US-00377268.  
 XX PF 28-FEB-2002; 2002US-0360651P.  
 XX PR 16-SEP-2002; 2002US-0411398P.  
 XX PR 20-SEP-2002; 2002US-0412341P.  
 XX PR 02-JAN-2003; 2003US-0437929P.  
 XX PA (PLEX-) PLEXXIKON INC.  
 XX PI Hirth K, Milburn MV;  
 XX PT DR WPI; 2004-642017/62.  
 XX PT Designing a ligand binding to a target molecule, comprises identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesizing ligand.  
 XX PT  
 XX PS Disclosure; SEQ ID NO 24; 186pp; English.  
 XX PA (BENN/) BENNER S A.  
 XX PI Benner SA;  
 XX DR WPI; 1999-570766/48.  
 XX PT Predicting the folded structure of proteins.  
 XX PS Disclosure; Col 253-256; 113pp; English.  
 CC Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for understanding the interaction of a protein with other molecules  
 CC  
 XX SQ Sequence 259 AA;

Query Match 100.0%; Score 45; DB 2; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 0.91; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSQL 9  
 248 TFDYLRSQL 256

Db

RESULT 13  
 ABR56203  
 ID ABR56203 standard; protein; 265 AA.  
 XX AC ABR56203;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).  
 XX KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme; Src-family protein tyrosine kinase; T-cell; immune response; mutein; mutant.

KW

RESULT 12  
 ADR88385

XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH  
Key Location/Qualifiers  
FT Misc-difference 128  
/note= "Wild-type D substituted with N. This position is  
364 in the full-length sequence (see ABR56202 for the  
wild-type full length sequence"  
FT Modified-site 158  
/note= "Phosphorylation site"  
XX  
PN WO2003020880-A2.  
XX  
PD 13-MAR-2003.  
XX  
PF 02-AUG-2002; 2002WO-US024546.  
XX  
PR 03-AUG-2001; 2001US-0310051P.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;  
XX  
WPI; 2003-300872/29.  
XX  
PT New crystalline polypeptide comprising ligand binding domain or catalytic  
domain of Lck protein, for determining three-dimensional structure of  
catalytic domain of Lck, has predetermined unit cell parameters.  
XX  
PT New crystalline polypeptide comprising ligand binding domain or catalytic  
domain of Lck protein, for determining three-dimensional structure of  
catalytic domain of Lck, has predetermined unit cell parameters.  
XX  
DR 2003-300872/29.  
XX  
DR Leung A, Ritter K;  
XX  
WPI; 2003-300872/29.  
XX  
PT New crystalline polypeptide comprising ligand binding domain or catalytic  
domain of Lck protein, for determining three-dimensional structure of  
catalytic domain of Lck, has predetermined unit cell parameters.  
XX  
PS Example 1; Fig 3; 994pp; English.  
XX  
CC The present invention relates to a crystalline polypeptide (I),  
comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)  
protein. Lck is a Src-family protein tyrosine kinase expressed primarily  
in T-cells and plays an essential role in immune response. (I) is useful  
for identifying a compound which is an inhibitor of human Lck protein.  
CC The present sequence is a mutated fragment of the human Lck sequence,  
which approximately comprises the catalytic domain  
XX  
SQ Sequence 265 AA;  
Query Match 100.0%; Score 45; DB 7; Length 265;  
Best Local Similarity 100.0%; Pred. No. 0.93; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TFDYLRSQL 9  
Db 250 TFDYLRSQL 258  
XX  
RESULT 14  
ABR56204  
ID ABR56204 standard; protein; 271 AA.  
XX  
AC ABR56204;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).  
XX  
KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;  
KW Src-family protein tyrosine kinase; T-cell; immune response; muttein;  
KW mutant.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Location/Qualifiers  
FT Misc-difference 134  
/note= "Wild-type D substituted with N. This position is  
364 in the full-length sequence (see ABR56202 for the  
wild-type full length sequence"  
XX  
PN WO2005028624-A2.  
XX  
PD 31-MAR-2005.  
XX  
PF 15-SEP-2004; 2004WO-US030360.  
XX  
PR 15-SEP-2003; 2003US-0503277B.  
XX  
PA (PLEX-) PLEXXIKON INC.  
XX  
PI Artis DR, Bremer RE, Gillette SJ, Hurt CR, Ibrahim PL;  
PI Zuckerman RL;  
XX  
DR WPI; 2005-273155/28.

XX  
PT New scaffold library used for identifying and developing ligands for protein kinases and treating kinase associated disorders e.g. cancer,  
PT comprises set of compounds comprising N-heterocyclic compounds.  
XX  
PS Disclosure; Page 170-174; 236pp; English.

CC The invention relates to a new kinase scaffold library comprises at least 1 set of compounds, each set comprising at least 1 N-heterocyclic compound of formulae (I)-(VII) given in the specification. Also included are a system for fitting compounds in binding sites of protein kinases (comprising an electronic kinase scaffold, and a scaffold library comprising at least 1 collection of electronic representations of (I)-(VII), where the scaffold library is embedded in a computer device and the electronic representations of the compounds can be selectively retrieved and functionally connected with computer software adapted to fit electronic representations of compounds in an electronic representation of a binding site of a kinase), obtaining improved ligands binding to a protein kinase (which comprises determining if a derivative of (I)-(VII) binds to the kinase with greater affinity and/or specificity than (I)-(VII)), developing ligands specific for a particular kinase (which comprises determining if a derivative of (I)-(VII) that binds to kinases has greater for specificity for the particular kinase than (I)-(VII)), developing ligands binding to a kinase (which comprises determining the orientation of at least 1 molecular scaffold of (I)-(VII) in co-crystals with the kinase, identifying chemical structures of the scaffolds, that, when modified, change the binding affinity and/or specificity between the scaffold and kinase and synthesizing a ligand in which at least 1 chemical structure of the scaffold is modified), developing ligands with increased specificity on a kinase (which comprises testing a derivative of a kinase binding compound (I)-(VII) for increased specificity on the kinase); identifying a ligand binding to a kinase (which comprises determining if a derivative compound including a core structure (I)-(VII) binds to the kinase with changed binding affinity and/or specificity); a co-crystal of a kinase and a binding compound (I)-(VII), preparation of co-crystals of Pim-1 with (I)-(VII), identifying potential kinase binding compounds (which comprises fitting electronic representations of (I)-(VII) in an electronic representation of a kinase binding site), attaching a kinase binding compound to an attachment component (which comprises identifying energetically allowed sites for attachment of the component on a kinase binding compound (I)-(VII) and attaching the compound or derivative to the attachment component at the allowed site), modified compounds (comprising (I)-(VIII) with an attached linker group, and developing a ligand for a kinase comprising conserved residues matching at least one of Pim-1 residues 49, 52, 67, 121, 128 and 186 which comprises determining if (I)-(VII) binds to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet, vascular endothelial growth factor receptor, endothelial growth factor receptor, cKit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold library is used for identifying and developing ligands binding to kinases, for modulating kinase activity and for treating disease condition associated with abnormal kinase activity e.g. cancer, inflammatory disease. The method identifies improved ligands binding to a kinase resulting in ligands having high affinity and specificity towards kinase. The co-crystals of kinase and the binding compound are of sufficient size and quality to allow structural determination of at least 2 Angstroms. The present sequence is a catalytic domain from a PIM-like kinase. NOTE: It is not clear whether the sequence as presented represents a continuous amino acid sequence.

XX Sequence 279 AA;

Query Match 100.0%; Score 45; DB 9; Length 279;  
Best Local Similarity 100.0%; Pred. No. 0.99; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSVL 9  
Db 256 TFDYLRSVL 264

ID AAY76750 standard; protein; 346 AA.  
XX AC AAY76750;  
XX DT 17-APR-2000 (first entry)  
XX DE Human protein kinase homologue, PKH-3.  
XX KW Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS; autoimmune disorder; inflammatory disorder; reproductive defect; asthma; diabetes mellitus; infertility; ovulatory defect; endometriosis; polycystic ovary syndrome.  
XX OS Homo sapiens.  
XX PN US6013455-A.  
XX PD 11-JAN-2000.  
XX PR 15-OCT-1998; 98US-00173581.  
XX PA (INCY-) INCYTE PHARM INC.  
XX Hillman JL, Yue H, Yang YT, Corley NC, Gorgone GA, Azimzai Y; Lu DAM, Bandman O, Guegler KJ;  
XX DR WPI; 2000-136321/12.  
XX PT Nucleic acids encoding a human protein kinase homolog useful for preventing, diagnosing and treating cancer, autoimmune/inflammatory disorders and reproductive defects.  
XX PS Claim 1; Col 47-50; 38pp; English.  
CC This sequence represents a human protein kinase homolog (PKH) of the invention. The PKH sequences may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PKH expression such as cancers, autoimmune/inflammatory disorders and reproductive defects. They may be used to treat disorders associated with decreased PKH expression such as cancers (e.g. lymphoma, melanoma and cancers of the breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS, asthma and diabetes mellitus), and reproductive defects (e.g. infertility, ovulatory defects, endometriosis and polycystic ovary syndrome). The DNA may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PKH by expressing inactive proteins or to supplement the patient's own production of PKH polypeptides. Additionally, the DNA may be used to produce PKH, according to standard recombinant DNA methodology, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. Conversely, antisense nucleic acid molecules may be administered to down regulate PKH expression by binding with the cells own PKH genes and preventing their expression. The DNA, and antisense sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence which patients may be in need of restorative therapy. They may also be used to study the expression and function of PKH polypeptides and their role in metabolism. The PKH polypeptides may be used as antigens in the production of antibodies against PKH and in assays to identify modulators (agonists and antagonists) of PKH expression and activity. The anti-PKH antibodies and PKH antagonists may also be used to down regulate PKH expression and activity. The anti-PKH antibodies may also be used as diagnostic agents for detecting the presence of PKH polypeptides in samples.  
XX SQ Sequence 346 AA;  
Query Match 100.0%; Score 45; DB 3; Length 346;  
Best Local Similarity 100.0%; Pred. No. 1.3; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16 AAY76750

Qy	1 TFDYIILRSVL 9	Db	323 TFDYIILRSVL 331
Db	323 TFDYIILRSVL 331		
RESULT 17			
AAE06208			
ID AAE06208	standard; protein; 346 AA.		
XX			
AC AAE06208;			
XX			
DT 25-SEP-2001	(first entry)		
XX			
DE Human protein kinase homolog-3 (PKH-3).			
XX			
KW Human; protein kinase homolog-3; PKH-3; cytostatic; protein therapy; vaccine; immunosuppressive; antisclerotic; antiabortive; adenocarcinoma; Acquired immune deficiency Syndrome; AIDS; melanoma; cancer; bone; liver; breast; autoimmune disorder; multiple sclerosis; drug screening; anaemia; Crohn's disease; ectopic pregnancy; tubal disease; inflammatory disorder; reproductive disorder; polycystic ovary syndrome; asthma.			
XX			
OS Homo sapiens.			
XX			
FH Key Location/Qualifiers			
FT Region 125. .333 /note= "Signature sequence"			
XX			
PN US6264947-B1.			
XX			
PD 24-JUL-2001.			
XX			
PF 20-OCT-1999; 99US-00420915.			
XX			
PR 15-OCT-1998; 98US-00173581.			
XX			
PA (INCY-) INCYTE GENOMICS INC.			
XX			
PT Bandman O, Tang YT, Hillman JL, Yue H, Guegler KJ, Corley NC;			
PI Gorgone GA, Azimzai Y, Lu DAM;			
XX			
DR N-PSDB; AAD11845.			
XX			
PT Human protein kinase proteins and homologs, useful for preventing, diagnosing and treating cancers, autoimmune/inflammatory disorders and reproductive disorders.			
PT XX			
PS Claim 1; Col 47-50; 38pp; English.			
XX			
CC The present sequence is human protein kinase homolog-3 (PKH-3). Human protein kinase homologs (PKH) and their cDNA molecules are used in the prevention, diagnosis and treatment of diseases associated with increased or decreased expression of PKH. Examples of such disorders include, cancer (e.g. adenocarcinoma, melanoma and bone, breast and liver cancer), autoimmune/inflammatory disorders (e.g. Acquired Immune deficiency Syndrome (AIDS), anaemia, asthma, Crohn's disease and multiple sclerosis) and reproductive disorders (e.g. tubal disease, ectopic pregnancy and polycystic ovary syndrome). PKH, its catalytic or immunogenic fragment are used for screening libraries of compounds in any of the drug screening techniques. PKH nucleic acids are used to generate hybridisation probes useful in mapping the naturally occurring genomic sequences. PKH are also used as antigens in the production of antibodies against protein kinases (PK) and in assays to identify modulators of PK expression and activity. PKH is also used in protein therapy			
CC XX			
SQ Sequence 346 AA;			
Query Match 100.0%; Score 45; DB 4; Length 346;			
Best Local Similarity 100.0%; Pred. No. 1.3;			
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
1 TFDYIILRSVL 9			

treatment. The polypeptide and polynucleotide are used for treating acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, haemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, infertility, including tubal disease, protozoal, and helminthic infections, infertility, disruptions of the oestrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis. The polypeptides of the invention can be used for gene therapy. This sequence represents a PKH from clone ID 507669 isolated from TMLR3DT02, a library constructed using RNA isolated from non-adherent peripheral blood mononuclear cells collected from a pool of male and female donors

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX

treatment. The polypeptide and polynucleotide are used for treating acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, haemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, infertility, including tubal disease, protozoal, and helminthic infections, infertility, disruptions of the oestrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis. The polypeptides of the invention can be used for gene therapy. This sequence represents a PKH from clone ID 507669 isolated from TMLR3DT02, a library constructed using RNA isolated from non-adherent peripheral blood mononuclear cells collected from a pool of male and female donors

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX  
 CC The sequence consists of the N-terminal amino acids of the beta-  
 CC galactosidase gene fused with the lck gene. It is produced by E.coli  
 CC transformed with a recombinant vector (see AAQ13983). It is useful for  
 producing an antibody specifically immunoreactive with only a lck gene-  
 CC derived polypeptide in T cells. The antibody may recognise lck gene-  
 XX derived polypeptides in human cells  
 SQ Sequence 417 AA;

Query Match 100.0%; Score 45; DB 2; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TFDYLRSQL 9  
 Db 394 TFDYLRSQL 402

RESULT 21  
 ADC99048  
 ID ADC99048 standard; protein; 458 AA.

XX  
 AC ADC99048;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human KPP protein - SEQ ID 1.  
 XX  
 KW anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;  
 KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;  
 KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;  
 KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;  
 KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;  
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
 KW virucide; protozoocide; fungicide; kinase; phosphatase; KPP;  
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
 KW cancer; developmental; mental retardation; neurological;  
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;  
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
 KW helminthic infection; transgenic; gene therapy; human; enzyme.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003033680-A2.  
 XX  
 PD 24-APR-2003.  
 XX  
 PF 17-OCT-2002; 2002WO-US033723.  
 PR 19-OCT-2001; 2001US-0345474P.  
 PR 02-NOV-2001; 2001US-0343910P.  
 PR 13-NOV-2001; 2001US-0333098P.  
 PR 16-NOV-2001; 2001US-0332424P.  
 PR 30-NOV-2001; 2001US-0334288P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Bandman O, Baughn MR, Bechha SD, Borowsky ML, Duggan BM;  
 PI Emerling BM, Forsythe RJ, Gandhi AR, Gorvard AE, Griffin JA;  
 PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;  
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;  
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;  
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;  
 PI Zebarradian Y;  
 DR WPI; 2003-403214/38.  
 DR N-PSDB; ADC99100.

XX  
 CC New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.

XX  
 PS Claim 1; SEQ ID NO 1; 424pp; English.  
 XX  
 CC The invention relates to a novel isolated polypeptide which is a human  
 kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP protein of the  
 CC invention.  
 XX  
 SQ Sequence 458 AA;

Query Match 100.0%; Score 45; DB 7; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TFDYLRSQL 9  
 Db 435 TFDYLRSQL 443

RESULT 22  
 AAE21689  
 ID AAE21689 standard; protein; 502 AA.  
 XX  
 AC AAE21689;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 16-JUL-2002 (first entry)  
 XX  
 DE Fugu rubripes lymphocyte kinase (LCK) protein.  
 XX  
 KW T-lymphocyte modulator; autoimmune disorder; graft rejection;  
 KW graft-versus-host disease; viral infection; lymphocyte kinase; LCK.  
 XX  
 OS Takifugu rubripes.  
 XX  
 PN WO200218619-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PF 16-AUG-2001; 2001WO-IL000765.  
 XX  
 PR 01-SEP-2000; 2000US-0229326P.  
 XX  
 PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
 PA (EHRL/) EHRLICH G.  
 XX  
 PI Brenner S, Venkatesh B, Tan VH;  
 XX  
 DR WPI; 2002-329781/36.  
 DR N-PSDB; AAD34173.

XX  
 CC New nucleic acids, useful for regulating T-cell mediated immune  
 PT responses, e.g., suppressing T-lymphocytes in subjects with autoimmune  
 PT disorders, or enhancement in those with viral infections, comprises novel  
 PT T-cell active promoters.  
 XX  
 PS Example 2; Page 55-57; 67pp; English.

XX  
 CC The invention relates to an isolated nucleic acid which includes a  
 CC promoter sequence being transcriptionally functional in a T-lymphocyte  
 CC undergoing activation and transcriptionally less functional in the T-  
 CC lymphocyte prior to the activation. The nucleic acid is useful for  
 CC regulating T-cell mediated immune responses in mammals. Nucleic acid  
 PT molecules of the invention may be used to suppress or eliminate T-

CC lymphocytes undergoing activation to suppress T-lymphocyte mediated  
 CC immune response in individuals suffering from immune disorders, e.g.  
 CC autoimmune disorders such as graft rejection or graft-versus-host  
 disease. They may also be used to enhance T-lymphocyte mediated immune  
 response in individual suffering from, e.g. viral infection. The present  
 CC sequence is Fugu rubripes Lymphocyte kinase (LCK) protein. (Updated on 29  
 CC -AUG-2003 to standardise OS field)  
 XX Sequence 502 AA;

Qy	1 TFDYLRSQL 9
Db	485 TFDYLRSQL 493

Query Match 100.0%; Score 45; DB 5; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TFDYLRSQL 9  
 481 TFDYLRSQL 489

RESULT 23

AAB37700	ID AAB37700 standard; protein; 508 AA..
XX	
AC AAB37700;	
XX	
DT 02-MAR-2001 (first entry)	
XX	
DE Human Lymphocyte kinase.	
XX	
KW Human; Lymphocyte kinase; protein co-ordinate data; lck; crystal.	
XX	
OS Homo sapiens.	
XX	
PN WO2003016475-A2.	
XX	
PD 27-FEB-2003.	
XX	
PF 14-AUG-2002; 2002WO-US025765.	
XX	
PR 14-AUG-2001; 2001US-0312147P.	
XX	
PR 01-NOV-2001; 2001US-0346382P.	
XX	
PR 26-NOV-2001; 2001US-0333347P.	
XX	
PA (GEHO ) GEN HOSPITAL CORP.	
PA (FARB ) BAYER AG.	
XX	
PD 23-NOV-2000.	
XX	
PF 19-MAY-2000; 2000WO-US013881.	
XX	
PR 19-MAY-1999; 99US-0134965P.	
XX	
PA (KINE-) KINETIX PHARM INC.	
XX	
PI Zhu X;	
XX	
DR WPI; 2000-687708/67.	
XX	
PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.	
XX	
PS Claim 1; Page 434-5; 438pp; English.	
XX	
CC The present invention relates to a crystal of a protein-ligand complex CC comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal CC diffracts X-rays so that the atomic coordinates of the protein-ligand CC complex can be determined to a resolution of greater than 5.0 Angstroms. CC The truncated lck used in the present invention comprises the globular CC core of the corresponding full-length lck. The present sequence is the CC full-length human lck protein. The crystal of the present invention may CC be used to identify kinase inhibitors in screening assays, in drug CC screening and drug design processes, to design, select or test inhibitors CC of kinase enzymes, where the inhibitors are used as therapeutics for the CC treatment and modulation of diseases, disease symptoms or the effect of CC other physiological events mediated by kinases, having one or more kinase CC enzymes involved in their pathology	
XX	
SQ Sequence 508 AA;	
Query Match 100.0%; Score 45; DB 3; Length 508; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

SQ	Sequence 508 AA;	CC	the specification) which is differentially expressed during pain. Note:
Query Match	100.0%; Score 45; DB 7; Length 508;	CC	The sequence data for this patent did not form part of the printed
Best Local Similarity	100.0%; Pred. No. 1.9;	CC	specification, but was obtained in electronic form directly from WIPO at
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	ftp.wipo.int/pub/published_pct_sequences.
Qy	1 TFDYLRSQL 9	SQ	Sequence 508 AA;
Db	485 TFDYLRSQL 493	Qy	1 TFDYLRSQL 9
RESULT 25		Db	485 TFDYLRSQL 493
ADE58799		Qy	1 TFDYLRSQL 9
ID ADE58799 standard; protein; 508 AA.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
AC ADE58799;		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
DT 29-JAN-2004 (first entry)		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
DE Human Protein P06239, SEQ ID NO 4686.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
KW Human; pain; neuronal tissue; gene therapy;		Db	485 TFDYLRSQL 493
KW spinal segmental nerve injury; chronic constriction injury; CCI;		Qy	1 TFDYLRSQL 9
KW spared nerve injury; SNI; Chung.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
OS Homo sapiens.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
PN WO2003016475-A2.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
PD 27-FEB-2003.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
PF 14-AUG-2002; 2002WO-US025765.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
PR 14-AUG-2001; 2001US-0312147P.		Db	485 TFDYLRSQL 493
PR 01-NOV-2001; 2001US-0346382P.		Qy	1 TFDYLRSQL 9
PR 26-NOV-2001; 2001US-0333347P.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
(GEHO ) GEN HOSPITAL CORP.		Db	485 TFDYLRSQL 493
PA (FARB ) BAYER AG.		Qy	1 TFDYLRSQL 9
XX		Db	485 TFDYLRSQL 493
PT Woolf C, D'urso D, Befort K, Costigan M;		Qy	1 TFDYLRSQL 9
XX		Db	485 TFDYLRSQL 493
DR WPI; 2003-268312/26.		Qy	1 TFDYLRSQL 9
XX		Db	485 TFDYLRSQL 493
PT New composition comprising two or more isolated polypeptides, useful for		Qy	1 TFDYLRSQL 9
PT preparing a medicament for treating pain in an animal.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
PS Claim 1; Page; 1017pp; English.		Db	485 TFDYLRSQL 493
XX		Qy	1 TFDYLRSQL 9
CC The invention discloses a composition comprising two or more isolated rat		Db	485 TFDYLRSQL 493
CC or human polynucleotides or a polynucleotide which represents a fragment,		Qy	1 TFDYLRSQL 9
CC derivative or allelic variation of the nucleic acid sequence. Also		Db	485 TFDYLRSQL 493
CC claimed are a vector comprising the novel polynucleotide; a host cell		Qy	1 TFDYLRSQL 9
CC comprising the vector, a method for identifying a nucleotide sequence		Db	485 TFDYLRSQL 493
CC which is differentially regulated in an animal subjected to pain and a		Qy	1 TFDYLRSQL 9
CC kit to perform the method, an array, a method for identifying an agent		Db	485 TFDYLRSQL 493
CC that increases or decreases the expression of the polynucleotide sequence		Qy	1 TFDYLRSQL 9
CC that is differentially expressed in neuronal tissue of a first animal		Db	485 TFDYLRSQL 493
CC subjected to pain, a method for identifying a compound which regulates		Qy	1 TFDYLRSQL 9
CC the expression of a polynucleotide sequence which is differentially		Db	485 TFDYLRSQL 493
CC expressed in an animal subjected to pain, a method for identifying a		Qy	1 TFDYLRSQL 9
CC compound that regulates the activity of one or more of the		Db	485 TFDYLRSQL 493
CC polynucleotides, a method for producing a pharmaceutical composition, a		Qy	1 TFDYLRSQL 9
CC method for identifying a compound or small molecule that regulates the		Db	485 TFDYLRSQL 493
CC activity in an animal of one or more of the polypeptides given in the		Qy	1 TFDYLRSQL 9
CC specification, a method for identifying a compound useful in treating		Db	485 TFDYLRSQL 493
CC pain and a pharmaceutical composition comprising the one or more		Qy	1 TFDYLRSQL 9
CC polypeptides or their antibodies. The polynucleotide or the compound that		Db	485 TFDYLRSQL 493
CC modulates its activity is useful for preparing a medicament for treating		Qy	1 TFDYLRSQL 9
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction		Db	485 TFDYLRSQL 493
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene		Qy	1 TFDYLRSQL 9
CC therapy). The sequence presented is a human protein (shown in Table 2 of		Db	485 TFDYLRSQL 493

CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TFDYLRSQL 9  
 CC Db 485 TFDYLRSQL 493

CC Sequence 508 AA;

CC Query Match 100.0%; Score 45; DB 7; Length 508;  
 CC Best Local Similarity 100.0%; Pred. No. 1.9;  
 CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 T

**RESULT 27**  
 ID ADL34479  
 ADL34479 standard; peptide; 508 AA..  
 XX  
 AC  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human lymphocyte kinase (Lck) globular core.  
 XX  
 KW cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide; fungicide; nootropic; neuroprotective; kinase inhibitor; crystal; protein-ligand complex; lymphocyte kinase; Lck; Lck ligand; kinase inhibitor; therapeutic; kinase-mediated physiological event; cancer; autoimmunological; metabolic; inflammatory; infection; central nervous system degenerative disease; transplant rejection; human; globular core; protein co-ordinate data.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6589758-B1.  
 XX  
 PD 08-JUL-2003.  
 XX  
 PF 21-MAY-2001; 2001US-00862154.  
 XX  
 PR 19-MAY-2000; 2000US-0205510P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Zhu X;  
 XX  
 DR WPI; 2003-810380/76.  
 XX  
 PT Crystal of protein-ligand complex useful for identifying an inhibitor of lymphocyte kinase (Lck), comprises truncated Lck and a ligand.  
 PS Claim 1; SEQ ID NO 1; 295pp; English.

XX  
 CC The invention describes a crystal (I) of a protein-ligand complex (C) comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I) effectively diffracts x-rays for determination of atomic coordinates of (C) to a resolution of greater than 5.0 angstroms, and truncated Lck comprises a sequence (S1) of residues 225-508 of a 508 amino acid sequence, given in specification and retains the globular core of full-length Lck. (I) is useful in an inhibitor screening assay and to identify, design, select, and evaluate potential inhibitors of kinases that would be useful as therapeutics for diseases or symptoms of diseases that are associated with kinase-mediated physiological events. The inhibitors identified by the methods may also be useful for inhibition of kinase activity of one or more enzymes. The inhibitors are also useful for inhibiting the biological activity of any enzyme comprising greater than 90%, alternatively greater than 85%, or alternatively greater than 70% sequence homology with a kinase sequence. The inhibitors are useful for inhibiting the biological activity of any enzyme that binds ATP and thus for treating disease or disease symptoms mediated by any enzyme that binds ATP. The inhibitors are useful in inhibiting kinase activity and are useful in treating kinase-mediated disease or disease symptoms in a mammal, particularly a human e.g., cancer, autoimmunological, metabolic, inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central nervous system degenerative disease etc. The inhibitors are useful in treating or preventing diseases, including, transplant rejection etc. This is the amino acid sequence of a human lymphocyte kinase (Lck) polypeptide comprising the Lck globular core.

XX  
 SQ Sequence 508 AA;

Query Match 100.0%; Score 45; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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**RESULT 28**  
 ID ADS88148  
 TD ADS88148 standard; protein; 508 AA.  
 XX  
 AC  
 XX  
 DT 18-NOV-2004 (first entry)  
 DE Human protein of a TNF-alpha signalling pathway protein complex SeqID 3.  
 XX  
 KW protein complex; tumour necrosis factor-alpha signalling pathway; TNF-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antirheumatic; cytostatic; antibacterial; gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004035783-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PR 24-SEP-2003; 2003WO-EP050655.  
 XX  
 PR 26-SEP-2002; 2002EP-00021809.  
 XX  
 PR 10-FEB-2003; 2003EP-00100274.  
 XX  
 PA (CELL-) CELLZONE AG.  
 XX  
 PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;  
 PI Superti-Furga G, Kruse U;  
 XX  
 DR WPI; 2004-348460/32.  
 XX  
 PT New protein complex comprising at least one first and second protein of the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for diagnosing or treating inflammation, neurological diseases, infectious diseases or cancer.

XX  
 PS Example; SEQ ID NO 3; 1980pp; English.

XX  
 CC This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The present invention describes a protein complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as rheumatoid arthritis and inflammatory bowel disease; infectious diseases such as septic shock and bacterial infections; neurological diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirheumatic, cytostatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides siRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification to form novel complexes of the TNF-alpha signalling pathway of the invention.

XX  
 SQ Sequence 508 AA;

Query Match 100.0%; Score 45; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSVL 9  
 ||||| 9

Db 485 TFDYLRSQL 493

ABR58699  
ID ABR58699 standard; protein; 509 AA.  
XX  
AC ABR58699;  
XX

RESULT 29

XX

AAV49420

ID AAV49420 standard; protein; 509 AA.

XX

AC AAV49420;

XX

DT 13-MAR-2000 (first entry)

XX

DE PKA substrate, Src-family protein.

XX

KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;

XX

KW kinase substrate; immunosuppressive disorder; proliferative disease;

XX

KW HIV infection; AIDS; immunodeficiency; autoimmune disease;

XX

KW systemic lupus erythematosus; Src-family.

XX

OS Homo sapiens.

XX

PN WO9952315-A2.

XX

PR 02-DEC-1999.

XX

PF 27-MAY-1999; 99WO-GB001680.

XX

PR 27-MAY-1998; 98NO-00002419.

XX

PR 30-DEC-1998; 98US-0114240P.

XX

(LAUR-) LAURAS AS.

XX

PA (JONE/) JONES E L.

XX

PI Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V,

XX

PI Tasken K, Vang T, Altman A, Munshi A;

XX

DR WO9952315-A2.

XX

DR N-PSDB; AAZ46491.

XX

PT Altering the activity of protein kinase signaling pathways, used for

PT treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,

PT e.g. cancers or autoimmune diseases.

XX

PS Claim 23; Page 95-96; 111pp; English.

XX

PT The invention provides a novel method of altering the activity of the

CC protein kinase A (PKA) signaling pathway in a cell that comprises

CC altering the extent of phosphorylation of one or more PKA substrates, or

CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical

CC compositions containing a nucleic acid molecule that encodes a PKA

CC substrate, or fragment, precursor or functionally equivalent variant,

CC where the sequence is modified to alter its susceptibility to

CC phosphorylation by PKA can be used for treating a disorder exhibiting

CC abnormal PKA signaling activity, immunosuppressive disorders or

CC proliferative diseases. They can be used for treating e.g. HIV infection,

CC AIDS, common variable immunodeficiency or cancers. Conditions in which

CC upregulation of the PKA pathway is required, such as autoimmune disease,

CC e.g. systemic lupus erythematosus, may also be treated. The present

CC sequence represents a PKA substrate, wherein the substrate is in the Src-

CC family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tyk,

CC FYk, Src-1 or Src-2

XX

SQ Sequence 509 AA;

SQ Query Match 100.0%; Score 45; DB 3; Length 509;

SQ Best Local Similarity 100.0%; Pred. No. 1.9;

SQ Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9

Db 486 TFDYLRSQL 494

RESULT 30

Mon Jul 3 08:56:38 2006

us-10-062-257a-1.rag

Page 16

Search completed: June 29, 2006, 09:13:07  
Job time : 88.8313 secs

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## OM protein - protein search, using sw model

Run on: June 29, 2006, 09:13:45 ; Search time 13.3373 Seconds

(without alignments)  
64.927 Million cell updates/sec

Title: US-10-062-257A-1

Perfect score: 45

Sequence: 1 TFDYLRSQL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

PIR\_80:\*
 1: pir1:\*
 2: pir2:\*
 3: pir3:\*
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result NO.	Score	Query %	Match Length	DB ID	Description
1	45	100.0	509	1 I48845	protein-tyrosine k
2	45	100.0	509	1 OKHULK	protein-tyrosine k
3	41	91.1	512	1 A39719	protein-tyrosine k
4	41	91.1	512	1 I56160	protein-tyrosine k
5	41	91.1	512	1 TVHULY	protein-tyrosine k
6	37	82.2	379	2 AF2409	mannosyl transferase
7	37	82.2	509	1 TVHAST	protein-tyrosine k
8	37	82.2	606	2 JC5604	ABC-transporting protein-kaurene synthase
9	37	82.2	789	2 T09672	lipoic acid synthase
10	36	80.0	308	2 C81658	probable chloroquione
11	36	80.0	311	2 F71500	probable lipoate s
12	36	80.0	507	1 A39939	protein-tyrosine k
13	36	80.0	2708	2 T09079	probable tyrosine kinase
14	36	80.0	2819	2 T09080	probable chloroquione
15	35	77.8	157	2 T27697	VPS29-like phosphotyrosine protein
16	35	77.8	503	1 JQ1321	probable tyrosine kinase
17	35	77.8	503	1 TVMSHC	probable tyrosine kinase
18	35	77.8	505	1 TVHUHC	probable tyrosine kinase
19	35	77.8	877	2 H71647	alanine-tRNA ligase
20	34	75.6	211	2 S12252	self incompatibility
21	34	75.6	330	1 AC0223	flagellar motor subunit
22	34	75.6	331	2 F90963	flagellar motor subunit
23	34	75.6	331	2 H64957	flagellar motor subunit
24	34	75.6	708	2 T03835	vaca protein - sili
25	33	73.3	113	2 G90223	DNA-directed RNA polymerase
26	33	73.3	223	2 F83703	D-amino-acid oxidase
27	33	73.3	345	1 JH0185	hypothetical protein
28	33	73.3	399	2 B96567	hypothetical protein
29	33	73.3	499	1 A40092	hypothetical protein

30 33 73.3 505 2 I37206  
 31 33 73.3 595 2 S72537  
 32 33 73.3 695 2 S66662  
 33 33 73.3 1010 2 T37667  
 34 33 73.3 286 2 S45389  
 35 32 71.1 286 2 G65082  
 36 32 71.1 371 2 F84826  
 37 32 71.1 392 2 S04205  
 38 32 71.1 405 2 T09359  
 39 32 71.1 448 2 S56260  
 40 41 71.1 451 2 T16481  
 41 41 71.1 499 2 H83254  
 42 42 71.1 536 2 S33569  
 43 32 71.1 505 2 H95946  
 44 32 71.1 517 2 A43807  
 45 32 71.1 517 2 S24547  
 46 32 71.1 663 1 TVMVR  
 47 32 71.1 978 2 G75516  
 48 32 71.1 600 2 F71434  
 49 32 71.1 663 1 TVHUF  
 50 51 71.1 1283 2 R28812  
 51 52 71.1 1465 2 A70199  
 52 53 71.1 1465 2 AE0255  
 53 52 71.1 1465 2 B87263  
 54 53 71.1 1465 2 A53291  
 55 54 71.1 1465 2 T03086  
 56 55 71.1 1465 2 T25026  
 57 56 71.1 1465 2 JQ1752  
 58 57 71.1 1465 2 C86539  
 59 58 71.1 1465 2 C82728  
 60 59 71.1 1465 2 C82728  
 61 60 71.1 1465 2 C82728  
 62 61 71.1 1465 2 C82728  
 63 62 71.1 1465 2 C82728  
 64 63 71.1 1465 2 C82728  
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 66 65 71.1 1465 2 C82728  
 67 66 71.1 1465 2 C82728  
 68 67 71.1 1465 2 C82728  
 69 68 71.1 1465 2 C82728  
 70 69 71.1 1465 2 C82728  
 71 70 71.1 1465 2 C82728  
 72 71 71.1 1465 2 C82728  
 73 72 71.1 1465 2 C82728  
 74 73 71.1 1465 2 C82728  
 75 74 71.1 1465 2 C82728  
 76 75 71.1 1465 2 C82728  
 77 76 71.1 1465 2 C82728  
 78 77 71.1 1465 2 C82728  
 79 78 71.1 1465 2 C82728  
 80 79 71.1 1465 2 C82728  
 81 80 71.1 1465 2 C82728  
 82 81 71.1 1465 2 C82728  
 83 82 71.1 1465 2 C82728  
 84 83 71.1 1465 2 C82728  
 85 84 71.1 1465 2 C82728  
 86 85 71.1 1465 2 C82728  
 87 86 71.1 1465 2 C82728  
 88 87 71.1 1465 2 C82728  
 89 88 71.1 1465 2 C82728  
 90 89 71.1 1465 2 C82728  
 91 90 71.1 1465 2 C82728  
 92 91 71.1 1465 2 C82728  
 93 92 71.1 1465 2 C82728  
 94 93 71.1 1465 2 C82728  
 95 94 71.1 1465 2 C82728  
 96 95 71.1 1465 2 C82728  
 97 96 71.1 1465 2 C82728  
 98 97 71.1 1465 2 C82728  
 99 98 71.1 1465 2 C82728  
 100 100 71.1 1465 2 C82728  
 30 33 73.3 505 2 I37206  
 31 33 73.3 595 2 S72537  
 32 33 73.3 695 2 S66662  
 33 33 73.3 1010 2 T37667  
 34 33 73.3 286 2 S45389  
 35 32 71.1 286 2 G65082  
 36 32 71.1 371 2 F84826  
 37 32 71.1 392 2 S04205  
 38 32 71.1 405 2 T09359  
 39 32 71.1 448 2 S56260  
 40 41 71.1 451 2 T16481  
 41 41 71.1 499 2 H83254  
 42 42 71.1 536 2 S33569  
 43 32 71.1 505 2 H95946  
 44 32 71.1 517 2 A43807  
 45 32 71.1 517 2 S24547  
 46 32 71.1 663 1 TVMVR  
 47 32 71.1 978 2 G75516  
 48 32 71.1 600 2 F71434  
 49 32 71.1 663 1 TVHUF  
 50 51 71.1 1283 2 R28812  
 51 52 71.1 1465 2 A70199  
 52 53 71.1 1465 2 AE0255  
 53 54 71.1 1465 2 B87263  
 54 55 71.1 1465 2 A53291  
 55 56 71.1 1465 2 T03086  
 56 57 71.1 1465 2 T25026  
 57 58 71.1 1465 2 JQ1752  
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 62 63 71.1 1465 2 C82728  
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 69 70 71.1 1465 2 C82728  
 70 71 71.1 1465 2 C82728  
 71 72 71.1 1465 2 C82728  
 72 73 71.1 1465 2 C82728  
 73 74 71.1 1465 2 C82728  
 74 75 71.1 1465 2 C82728  
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 77 78 71.1 1465 2 C82728  
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 84 85 71.1 1465 2 C82728  
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 86 87 71.1 1465 2 C82728  
 87 88 71.1 1465 2 C82728  
 88 89 71.1 1465 2 C82728  
 89 90 71.1 1465 2 C82728  
 90 91 71.1 1465 2 C82728  
 91 92 71.1 1465 2 C82728  
 92 93 71.1 1465 2 C82728  
 93 94 71.1 1465 2 C82728  
 94 95 71.1 1465 2 C82728  
 95 96 71.1 1465 2 C82728  
 96 97 71.1 1465 2 C82728  
 97 98 71.1 1465 2 C82728  
 98 99 71.1 1465 2 C82728  
 99 100 71.1 1465 2 C82728  
 30 33 73.3 505 2 I37206  
 31 33 73.3 595 2 S72537  
 32 33 73.3 695 2 S66662  
 33 33 73.3 1010 2 T37667  
 34 33 73.3 286 2 S45389  
 35 34 73.3 331 2 G90223  
 36 34 73.3 331 2 F83703  
 37 34 73.3 331 2 JH0185  
 38 34 73.3 331 2 B96567  
 39 34 73.3 331 2 A40092  
 40 35 73.3 331 2 A11736  
 41 35 73.3 331 2 A1227  
 42 35 73.3 331 2 AE1580  
 43 35 73.3 331 2 F90963  
 44 35 73.3 331 2 TVHUF  
 45 35 73.3 331 2 H71647  
 46 35 73.3 331 2 S12252  
 47 35 73.3 331 2 AC0223  
 48 35 73.3 331 2 TVMSHC  
 49 35 73.3 331 2 T09079  
 50 35 73.3 331 2 T09080  
 51 35 73.3 331 2 T27697  
 52 35 73.3 331 2 F97184  
 53 35 73.3 331 2 S54585  
 54 35 73.3 331 2 T19562  
 55 35 73.3 331 2 PN0114  
 56 35 73.3 331 2 S51600  
 57 35 73.3 331 2 T25887  
 58 35 73.3 331 2 T12725  
 59 35 73.3 331 2 E75196  
 60 35 73.3 331 2 E83332  
 61 35 73.3 331 2 E4562  
 62 35 73.3 331 2 T5272  
 63 35 73.3 331 2 P0114  
 64 35 73.3 331 2 S5272  
 65 35 73.3 331 2 S5272  
 66 35 73.3 331 2 S5272  
 67 35 73.3 331 2 S5272  
 68 35 73.3 331 2 S5272  
 69 35 73.3 331 2 S5272  
 70 35 73.3 331 2 S5272  
 71

## ALIGNMENTS

RESULT 1

I48845 protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse  
 N;Alternate names: p56; protein-tyrosine kinase tck  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text\_change 05-Oct-2004  
 C;Accession: I48845; A23539; T57629; I77452  
 R;Voronova, A.F.; Sefton, B.M.  
 Nature 319, 682-685, 1986  
 A;Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote  
 A;Reference number: I48845; MUID:86146842; PMID:3081813  
 A;Accession: I48845  
 A;Molecule type: mRNA  
 A;Residues: 1-509 <VOR1>  
 A;Cross-references: UNIPROT:Q91X65; UNIPARC:UPI00000418D; EMBL:X03533; NID:954813; PIDN  
 R;Marth, J.D.; Peet, R.; Krebs, E.G.; Perlmutter, R.M.  
 Cell 43, 393-404, 1985  
 A;Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpres  
 A;Reference number: A23639; MUID:86079521; PMID:2416464  
 A;Accession: A23639  
 A;Molecule type: mRNA  
 A;Residues: 1-282, 'VP', 285-509 <MAR>  
 A;Cross-references: UNIPARC:UPI0000172586; GB:M12056; NID:g198763  
 A;Note: the sequence is revised in GenBank entry MUSLCK, release 116.0., (PIDN:AAB59674.1  
 R;Voronova, A.F.; Adler, H.T.; Sefton, B.M.  
 Mol. Cell. Biol. 7, 4407-4413, 1987  
 A;Title: Two lck transcripts containing different 5' untranslated regions are present in  
 A;Reference number: I57629; MUID:88142832; PMID:3501824  
 A;Accession: I57629  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-11 <VOR>  
 A;Cross-references: UNIPARC:UPI000016CE9D; GB:M18098; NID:g198766; PIDN:AAA39421.1; PID:  
 R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.  
 Mol. Cell. Biol. 8, 3058-3064, 1988  
 A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel  
 A;Reference number: I57636; MUID:89096891; PMID:2850479  
 A;Accession: I77452  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-35, 'VR' <GAR>  
 A;Cross-references: UNIPARC:UPI000016CE9E; GB:M21511; NID:g198768; PIDN:AAA39422.1; PID:  
 C;Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro  
 F;68-116/Domain: SH3 homology <SH3>  
 F;127-224/Domain: SH2 homology <SH2>  
 F;243-501/Domain: protein kinase homology <KIN>  
 F;251-259/Region: protein kinase ATP-binding motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;273/Active site: Lys #status predicted  
 F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred  
 Query Match 100.0% Score 45; DB 1; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 0.3%;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

OKHULK protein-tyrosine kinase (EC 2.7.1.112) lck - human  
 N;Alternate names: kinase-related transforming protein (lck)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 05-Oct-2004  
 C;Accession: JQ0152; S07822; S07200; S01879; S07143; A32797; I57636  
 R;Rouer, E.; Van Huynh, T.; de Souza, S.L.; Lang, M.C.; Fischer, S.; Benarous, R.

Gene 84, 105-113, 1989  
 A;Title: Structure of the human lck gene: differences in genomic organisation within src  
 A;Reference number: JQ0152; MUID:90108697; PMID:2558056  
 A;Accession: JQ0152  
 A;Molecule type: DNA  
 A;Residues: 1-509 <ROU>  
 A;Cross-references: UNIPROT:P06239; UNIPARC:UPI0000151F17; EMBL:X14053  
 R;Perlmutter, R.M.; Marth, J.D.; Lewis, D.B.; Peet, R.; Ziegler, S.F.; Wilson, C.B.  
 J. Cell. Biochem. 38, 117-126, 1988  
 A;Title: Structure and expression of lck transcripts in human lymphoid cells.  
 A;Reference number: S07822; MUID:89123626; PMID:3265417  
 A;Accession: S07822  
 A;Molecule type: mRNA  
 A;Residues: 1-86, 'P', 88-509 <PER>  
 A;Cross-references: UNIPARC:UPI0000163BD5; EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID  
 R;Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshihikai, Y.; Mak, T.W.  
 Eur. J. Immunol. 16, 1643-1646, 1986  
 A;Title: A human T cell-specific cDNA clone (YT16) encodes a protein with extensive homo  
 A;Reference number: S07200; MUID:87133831; PMID:3493153  
 A;Accession: S07200  
 A;Molecule type: mRNA  
 A;Residues: 1-205, 'ASAITPI', 212-257, 'RCGW', 262, 'TTT', 266, 'T', 268-281, 'AGRLP', 287-503, 'STI  
 A;Cross-references: UNIPARC:UPI000016B09E; EMBL:X05027; NID:g36807; PIDN:CAA28691.1; PID  
 R;Veillette, A.; Foss, F.M.; Sausville, E.A.; Bolen, J.B.; Rosen, N.  
 Oncogene Res. 1, 357-374, 1987  
 A;Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other nc  
 A;Reference number: S01879; MUID:88217332; PMID:2835736  
 A;Accession: S01879  
 A;Molecule type: mRNA  
 A;Residues: 368-471, 'H', 473-509 <WEI>  
 A;Cross-references: UNIPARC:UPI000016ABFC; EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID  
 R;Trevillyan, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Linna, T.J.  
 Biochim. Biophys. Acta 888, 286-295, 1986  
 A;Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56(LSTRA).  
 A;Reference number: S07143; MUID:87000726; PMID:3489486  
 A;Accession: S07143  
 A;Molecule type: mRNA  
 A;Residues: 'A', 376-509 <TRE>  
 A;Cross-references: UNIPARC:UPI000016AF39; EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID  
 R;Garvin, A.M.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W.  
 Mol. Cell. Biol. 9, 2173-2180, 1989  
 A;Title: Structure of the two promoters of the human lck gene: differential accumulation  
 A;Reference number: A32797; MUID:89313764; PMID:2787474  
 A;Accession: A32797  
 A;Molecule type: DNA  
 A;Residues: 1-35 <TAK>  
 A;Cross-references: UNIPARC:UPI000016ABFF; GB:M26692; NID:g341523; PIDN:AAA59503.1; PID:  
 R;Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.  
 Mol. Cell. Biol. 8, 3058-3064, 1988  
 A;Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cel  
 A;Reference number: I57636; MUID:89096891; PMID:2850479  
 A;Accession: I57636  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-35, 'VR' <RES>  
 A;Cross-references: UNIPARC:UPI000016ABFD; GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:  
 C;Comment: Protein tyrosine kinases play important roles in the control of cell growth ar  
 C;Genetics:  
 A;Gene: GDB:LCK  
 A;Cross-references: GDB:119360; OMIM:153390  
 A;Map position: 1p35-1p34.3  
 A;Introns: 35/3; 63/1; 93/2; 126/2; 161/1; 211/1; 262/1; 322/1; 347/3; 399/1; 443/1  
 C;Function:  
 A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP  
 C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
 C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho  
 F;2-509/Product: protein-tyrosine kinase lck #status predicted <MAT>  
 F;68-116/Domain: SH3 homology <SH3>  
 F;127-224/Domain: SH2 homology <SH2>  
 F;243-501/Domain: protein kinase homology <KIN>  
 F;251-259/Region: protein kinase ATP-binding motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;3,5/Binding site: palmitate (Cys) (covalent) #status predicted

F;273/Active site: Lys #status predicted  
 F;394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred  
 Query Match  
 Best Local Similarity 100.0%; Score 45; DB 1; Length 509;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TFDYLRSVL 9  
 Db 486 TFDYLRSVL 494

RESULT 3  
 A39719  
 protein-tyrosine kinase (EC 2.7.1.112) lyn, long splice form - mouse  
 N;Contains: protein-tyrosine kinase lyn, short splice form  
 C;Species: Mus musculus (house mouse)  
 C;Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text\_change 05-Oct-2004  
 C;Accession: A39719; B39719; A39750; B39750  
 R;Stanley, E.; Ralph, S.; Boulet, I.; Holtzman, D.A.; Lock, P.; Dunn, A.R.  
 Mol. Cell. Biol. 11, 3399-3406, 1991  
 A;Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.  
 A;Reference number: A39719; MUID:91260688; PMID:1710766  
 A;Accession: A39719  
 A;Molecule type: mRNA  
 A;Residues: 1-512 <STA1>  
 A;Cross-references: UNIPROT:P25911; UNIPARC:UPI000016CEBE; GB:M64608; NID:g198938; PIDN:  
 A;Accession: B39719  
 A;Molecule type: mRNA  
 A;Residues: 1-24,46-512 <STA2>  
 A;Cross-references: UNIPARC:UPI0000172584; GB:M64608  
 R;Yi, T.; Bolen, J.B.; Ihle, J.N.  
 Mol. Cell. Biol. 11, 2391-2398, 1991  
 A;Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids  
 A;Reference number: A39750; MUID:91203857; PMID:2017160  
 A;Accession: A39750  
 A;Molecule type: mRNA  
 A;Residues: 1-76, 'F', 78-160, 'I', 162-278, 'L', 280-390, 'I', 392-424, 'D', 426-512 <Y11>  
 A;Cross-references: UNIPARC:UPI000016CEBF; GB:M57696; NID:g198940; PIDN:AAA39471.1; PID:  
 A;Accession: B39750  
 A;Molecule type: mRNA  
 A;Residues: 1-24,46-76, 'F', 78-160, 'I', 162-278, 'L', 280-390, 'I', 392-424, 'D', 426-512 <Y12>  
 C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
 C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein  
 F;1-1/512/Product: protein-tyrosine kinase lyn, long splice form #status predicted  
 F;1-24,46-512/Domain: SH3 homology <SH3>  
 F;1-29-226/Domain: SH2 homology <SH2>  
 F;245-504/Domain: protein kinase ATP-binding motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;275/Active site: Lys #status predicted  
 F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred  
 Query Match  
 Best Local Similarity 91.1%; Score 41; DB 1; Length 512;  
 Matches 8; Conservative 88.9%; Pred. No. 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 4  
 156160  
 protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat  
 N;Contains: protein-tyrosine kinase lyn, splice form B  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text\_change 05-Oct-2004  
 C;Accession: I56160; I67811; I67812  
 R;Minoguchi, K.; Nishikata, H.; Siraganian, R.P.  
 J. Immunol. 150, 222, 1993

RESULT 4  
 156160  
 protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat  
 N;Contains: protein-tyrosine kinase lyn, splice form B  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text\_change 05-Oct-2004  
 C;Accession: I56160; I67811; I67812  
 R;Minoguchi, K.; Nishikata, H.; Siraganian, R.P.  
 J. Immunol. 150, 222, 1993

A;Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leukemia cells  
 A;Reference number: I56160  
 A;Accession: I56160  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-512 <MIN>  
 A;Cross-references: UNIPROT:Q07014; UNIPARC:UPI0000167AC2; GB:L14951; NID:g294582; PIDN:  
 R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.  
 Gene 138, 219-222, 1994  
 A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed in  
 A;Reference number: I53715; MUID:94171041; PMID:8125304  
 A;Accession: I67811  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-230, 'L', 232-307, 'A', 309-418, 'Y', 420-512 <RID1>  
 A;Cross-references: UNIPARC:UPI0000170BE3; GB:L14782; NID:g294578; PIDN:AAA20944.1; PID:  
 A;Note: in Genbank entry RATLYNBTYR, release 116.0, PIDN:AAA20945.1, the source is design  
 A;Accession: I67812  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-24,46-230, 'L', 232-307, 'A', 309-418, 'Y', 420-512 <RID2>  
 A;Cross-references: UNIPARC:UPI0000170BE2; GB:L14823; NID:g294580; PIDN:AAA20945.1; PID:  
 A;Note: in Genbank entry RATLYNBTYR, release 116.0, PIDN:AAA20945.1, the source is design  
 C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
 C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein  
 F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MAT>  
 F;2-24,46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT>  
 F;70-118/Domain: SH3 homology <SH3>  
 F;129-226/Domain: SH2 homology <SH2>  
 F;245-504/Domain: protein kinase homology <KIN>  
 F;253-261/Region: protein kinase ATP-binding motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;275/Active site: Lys #status predicted  
 F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred  
 Query Match  
 Best Local Similarity 91.1%; Score 41; DB 1; Length 512;  
 Matches 8; Conservative 88.9%; Pred. No. 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 5  
 TVHULY  
 protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - human  
 N;Contains: protein-tyrosine kinase lyn, splice form B  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text\_change 05-Oct-2004  
 C;Accession: A26719; D38268; PH0949; I53715  
 R;Yamashita, Y.; Fukushima, S.I.; Semb, K.; Sukegawa, J.; Miyajima, N.; Matsubara, K.;  
 Mol. Cell. Biol. 7, 237-243, 1987  
 A;Title: The Yes-related cellular gene lyn encodes a possible tyrosine kinase similar to  
 A;Reference number: A26719; MUID:87172710; PMID:3561390  
 A;Accession: A26719  
 A;Molecule type: mRNA  
 A;Residues: 1-512 <YAM>  
 A;Cross-references: UNIPROT:P07948; UNIPARC:UPI000013DADC; GB:MI6038; NID:g187268; PIDN:  
 R;Partanen, J.; Mackelae, T.P.; Alitalo, R.; Lehtovaeslaaho, H.; Alitalo, K.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990  
 A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.  
 A;Reference number: A38268; MUID:91062389; PMID:2247464  
 A;Accession: D38268  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 369-424 <PAR>  
 A;Cross-references: UNIPARC:UPI0000172583  
 R;Bielke, W.; Ziemiak, A.; Kappos, L.; Miescher, G.C.  
 Biochem. Biophys. Res. Commun. 186, 1403-1409, 1992  
 A;Title: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobl  
 A;Reference number: PH0949; MUID:92378604; PMID:1510669  
 A;Accession: PH0949

A;Molecule type: mRNA  
A;Residues: 369-424 <BIE>  
A;Cross-references: UNIPARC:UPI0000172583  
A;Experimental source: neuroblastoma SK-IN cell  
R;Rider, L.G.; Raben, N.; Miller, L.; Jelsema, C.  
Gene 138, 219-222, 1994  
A;Title: The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed in  
A;Reference number: I53715; MUID:94171041; PMID:8125304  
A;Accession: I53715  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-24, 46-512 <RID>  
A;Cross-references: UNIPARC:UPI000016AC37; GB:M79321; NID:g187270; PIDN:AAB50019.1; PID:  
A;Experimental source: splice form B  
C;Genetics:  
A;Gene: GDB:LYN  
A;Cross-references: GDB:120159; OMIM:165120  
A;Map position: 8q13-8qter  
C;Function:  
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP  
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
C;Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein  
tyrosine-specific protein kinase  
F;2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>  
F;2-24, 46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT>  
F;70-118/Domain: SH3 homology <SH3>  
F;129-226/Domain: SH2 homology <SH2>  
F;245-504/Domain: protein kinase homology <KIN>  
F;253-261/Region: protein kinase ATP-binding motif  
F;2/Modified site: myristylated amino end (GLY) (in mature form) #status predicted  
F;3/Binding site: palmitate (Cys) (covalent) #status predicted  
F;275/Active site: Lys #status Predicted  
F;397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred  
Query Match 91.1%; Score 41; DB 1; Length 512;  
Best Local Similarity 88.9%; Pred. No. 2;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TFDYLRSQL 9  
Db 489 TFDYLQSQL 497

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RESULT 6  
AF2409  
mannosyl transferase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AF2409  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AF2409  
A;Molecule type: DNA  
A;Status: preliminary  
A;Residues: 1-379 <KUR>  
A;Cross-references: UNIPROT:Q8YMU7; UNIPARC:UPI00000CEC79; GB:BA000019; PIDN:BAB76529.1;  
C;Genetics:  
A;Gene: all4830  
C;Superfamily: hypothetical protein sll1534

Query Match 82.2%; Score 37; DB 2; Length 379;  
Best Local Similarity 100.0%; Pred. No. 9; 6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TFDYLRSQL 7  
Db 124 TFDYLRSQL 130

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RESULT 7  
TVHAST  
protein-tyrosine kinase (EC 2.7.1.112) stk - Hydra attenuata  
C;Species: Hydra attenuata  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-Oct-2004  
C;Accession: A34094  
R;Bosch, T.C.G.; Unger, T.F.; Fisher, D.A.; Steele, R.E.  
Mol. Cell. Biol. 9, 4141-4151, 1989  
A;Title: Structure and expression of STK, a src-related gene in the simple metazoan Hydra  
A;Reference number: A34094; MUID:90066418; PMID:2479820  
A;Accession: A34094  
A;Molecule type: mRNA  
A;Residues: 1-509 <BOB>  
A;Cross-references: UNIPROT:P17713; UNIPARC:UPI000013610D; GB:M25245; NID:g159273; PIDN:I  
C;Genetics:  
A;Gene: stk  
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phos  
F;66-115/Domain: SH3 homology <SH2>  
F;126-218/Domain: SH2 homology <SH2>  
F;238-497/Domain: protein kinase homology <KIN>  
F;246-254/Region: protein kinase ATP-binding motif  
F;2/Modified site: myristylated amino end (GLY) (in mature form) #status predicted  
F;4/Binding site: palmitate (Cys) (covalent) #status predicted  
F;268/Active site: Lys #status predicted  
F;390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
Query Match 82.2%; Score 37; DB 1; Length 509;  
Best Local Similarity 77.8%; Pred. No. 13;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 TFDYLRSQL 9  
Db 482 TFDYLQGVL 490

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RESULT 8  
JC5604  
ABC-transporting peroxisomal membrane protein 69 - human  
C;Species: Homo sapiens (man)  
C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 05-Oct-2004  
C;Accession: JC5604  
R;Holzinger, A.; Kammerer, S.; Roscher, A.A.  
Biochem. Biophys. Res. Commun. 237, 152-157, 1997  
A;Title: Primary structure of human PMP69, a putative peroxisomal ABC-transporter.  
A;Reference number: JC5604; MUID:97410133; PMID:9266848  
A;Accession: JC5604  
A;Residues: 1-606 <HOL>  
A;Cross-references: UNIPROT:O14678; UNIPARC:UPI00004C4C8; DDBJ:AF009746; NID:g2343156;  
C;Comment: This protein is a heterodimer partner of peroxisomal protein 70 and plays a r  
C;Genetics:  
A;Map position: 14q24.3  
A;Keywords: ATP; nucleotide binding; P-loop; peroxisome  
F;404-594/Domain: ATP-binding cassette homology <ABC>  
F;421-428/Region: nucleotide-binding motif A (P-loop)

Query Match 82.2%; Score 37; DB 2; Length 606;  
Best Local Similarity 77.8%; Pred. No. 16;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 TFDYLRSQL 9  
Db 276 TFDYLGSIL 284

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RESULT 9  
T09672  
ent-kaurene synthase B (EC 2.5.1.-) - winter squash  
C;Species: Cucurbita maxima (winter squash)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T09672

R; Yamaguchi, S.; Saito, T.; Abe, H.; Yamane, H.; Murofushi, N.; Kamiya, Y.  
 Plant J, 10, 203-213, 1996  
 A; Title: Molecular cloning and characterization of a cDNA encoding the gibberellin biosy  
 A; Reference number: Z16814; MUID:96367664; PMID:8771778  
 A; Accession: T09672  
 A; Status: preliminary; translated from GB/EMBL/DDBJ  
 A; Molecule type: mRNA  
 A; Residues: 1-789 <YAM>  
 A; Cross-references: UNIPROT:Q39548; UNIPARC:UPI0000ACCF3; EMBL:U43904; NID:g1431869; PI  
 A; Experimental source: immature seeds  
 C; Function:  
 A; Description: catalyzes the conversion of copalyl diphosphate to ent-kaurene  
 A; Pathway: gibberellin biosynthesis  
 C; Superfamily: terpene synthase  
 C; Keywords: transferase  
 A; Note: terpene cyclase  
 C; Description: catalyzes the conversion of copalyl diphosphate to ent-kaurene  
 A; Pathway: gibberellin biosynthesis  
 C; Superfamily: terpene synthase  
 C; Keywords: transferase

RESULT 10

Query Match 82.2%; Score 37; DB 2; Length 789;  
 Best Local Similarity 87.5%; Pred. No. 21;  
 Matches 7; Conservative 1; Mismatches 0;  
 Indels 0; Gaps 0;

QY 2 FDYLRSVL 9  
 Db 253 FDYLRSLL 260

C81658 lipoic acid synthetase TC0847 [imported] - Chlamydia muridarum (strain Nigg)  
 C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
 C; Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 31-Dec-2004  
 C; Accession: C81658  
 R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
 A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
 A; Reference number: A81500; MUID:20150255; PMID:10684935  
 A; Accession: C81658  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-308 <TET>  
 A; Cross-references: UNIPROT:Q9PJ12; UNIPARC:UPI000057AA5; GB:AE002351; GB:AE002160; NID  
 C; Genetics:  
 A; Gene: TC0847  
 C; Superfamily: lipoyl synthase

Query Match 80.0%; Score 36; DB 2; Length 308;  
 Best Local Similarity 87.5%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TFDYLRSV 8  
 Db 263 TFDYVRSV 270

RESULT 11

F71500 probable lipoate synthetase - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
 C; Species: Chlamydia trachomatis  
 C; Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 31-Dec-2004  
 C; Accession: F71500  
 R; Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
 A; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac  
 A; Reference number: A71570; MUID:99000809; PMID:9784136  
 A; Accession: F71500  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-311 <ARN>  
 A; Cross-references: UNIPROT:Q84562; UNIPARC:UPI000012B6C5; GB:AE001326; GB:AE001273; NID  
 C; Genetics:

RESULT 12

A39939 protein-tyrosine kinase (EC 2.7.1.112) tkl [similarity] - chicken  
 N; Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen ass  
 C; Species: Gallus gallus (chicken)  
 C; Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 05-Oct-2004  
 C; Accession: A42126; A39939  
 R; Chow, L.M.; Ratcliffe, M.J.; Villette, A.  
 Mol. Cell. Biol. 12, 1226-1233, 1992  
 A; Title: tkl is the avian homolog of the mammalian lck tyrosine protein kinase gene.  
 A; Reference number: A42126; MUID:92186854; PMID:1545804  
 A; Accession: A42126  
 A; Molecule type: mRNA  
 A; Residues: 1-88 <CHO>  
 A; Cross-references: UNIPARC:UPI0000172587; GB:M85043  
 A; Experimental source: thymus, spleen  
 A; Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBIP:88833)  
 R; Strehardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987  
 A; Title: Additional member of the protein-tyrosine kinase family: the src-and lck-related  
 A; Reference number: A39939; MUID:88097370; PMID:3321053  
 A; Accession: A39939  
 A; Molecule type: mRNA  
 A; Residues: 52-507 <STR>  
 A; Cross-references: UNIPARC:UPI00001713B3; GB:J03579; NID:g212712; PID:AAA49081.1; PID:  
 C; Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
 C; Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phoi  
 F; 66-114/Domain: SH3 homology <SH3>  
 F; 125-222/Domain: SH2 homology <SH2>  
 F; 241-499/Domain: protein kinase homology <KIN>  
 F; 249-257/Region: protein kinase ATP-binding motif  
 F; 2/Modified site: myristylated amino end (GLY) (in mature form) #status predicted  
 F; 392,503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred  
 Query Match 80.0%; Score 36; DB 1; Length 507;  
 Best Local Similarity 66.7%; Pred. No. 21;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSV 9  
 Db 484 TFEYMKSVL 492

RESULT 13

T09079 probable chloroquine resistance protein CG2 (strain 7G8) - malaria parasite (Plasmodium  
 C; Species: Plasmodium falciparum  
 C; Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
 C; Accession: T09079  
 R; Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellens, T.E.  
 Cell 91, 593-603, 1997  
 A; Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant  
 A; Reference number: Z16556; MUID:98054002; PMID:9393853  
 A; Accession: T09079  
 A; Status: translated from GB/EMBL/DDBJ  
 A; Molecule type: DNA  
 A; Residues: 1-2708 <SUX>  
 A; Cross-references: UNIPROT:O15791; UNIPARC:UPI0000079A61; EMBL:AF030692; NID:g2642513;  
 C; Genetics:  
 A; Gene: cg2

C;Keywords: toxin resistance

Query Match 80.0%; Score 36; DB 2; Length 2708;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02; PIDN:C,  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FDYLRSVL 9  
Db 48 FDYLRSAL 55

RESULT 14

T09080 probable chloroquine resistance protein CG2 (strain HB3) - malaria parasite (Plasmodium C;Species: Plasmodium falciparum  
C;Accession: T09080  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: T09080  
R;Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellens, T.E.  
Cell 91, 593-603, 1997  
A;Title: Complex polymorphisms in an 330 kDa protein are linked to Chloroquine-resistant A;Reference number: JQ1321; MUID:92109719; PMID:1764064  
A;Accession: JQ1321  
A;Molecule type: mRNA  
A;Residues: 1-503 <OKA>  
A;Cross-references: UNIPROT:P50545; UNIPARC:UPI000012C350; GB:S74141; NID:g241436; PIDN:  
A;Experimental source: megakaryocyte  
R;Rema, V.; Swarup, G.  
submitted to the EMBL Data Library, December 1991  
A;Accession: S18974  
A;Reference number: S18974  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-50, 'V', 52-204, 'R', 206-305, 'T', 307-503 <REM>  
A;Cross-references: UNIPARC:UPI0000170BD7; EMBL:X62345; NID:g57581; PIDN:CAA44218.1; PID  
A;Accession: T09080  
A;Molecule type: DNA  
A;Residues: 1-2819 <SUX>  
A;Cross-references: UNIPROT:O15792; UNIPARC:UPI00000785E5; EMBL:AF030693; NID:g2642515;  
A;Experimental source: strain HB3; from Honduras  
C;Genetics:  
A;Gene: cg2  
C;Keywords: toxin resistance

Query Match 80.0%; Score 36; DB 2; Length 2819;  
Best Local Similarity 87.5%; Pred. No. 1.3e+02; PIDN:  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FDYLRSVL 9  
Db 48 FDYLRSAL 55

RESULT 15

T27697 VPS29-like phosphoesterase-related protein ZK1128.8 [similarity] - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Accession: T27697  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T27697  
R;Berk, M.  
submitted to the EMBL Data Library, January 1995  
A;Reference number: 220407  
A;Accession: T27697  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-157 <WIL>  
A;Cross-references: UNIPROT:Q9XW5; UNIPARC:UPI000007FB10; EMBL:Z47357; PIDN:CAA87426.1;  
A;Experimental source: clone ZK1128  
C;Genetics:  
A;Gene: CBSP:ZK1128.8  
A;Map position: 3  
A;Introns: 20/2; 68/3  
C;Superfamily: VPS29-like phosphoesterase-related protein; phosphoesterase core homology

Query Match 77.8%; Score 35; DB 2; Length 157;  
Best Local Similarity 75.0%; Pred. No. 9.6; PIDN:C,  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSV 8  
Db 15 TFDYLRTL 22

RESULT 16

JQ1321 protein-tyrosine kinase (EC 2.7.1.112) hck - rat

RESULT 17

TVMSHC protein-tyrosine kinase (EC 2.7.1.112) hck - mouse  
N;Alternate names: kinase-related transforming protein (bmk)  
C;Species: Mus musculus (house mouse)  
C;Accession: T27697  
C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 05-Oct-2004  
C;Accession: A27282; A39973  
R;Klemsz, M.J.; McKercher, S.R.; Maki, R.A.  
Nucleic Acids Res. 15, 960, 1987  
A;Title: Nucleotide sequence of the mouse hck gene.  
A;Reference number: A27282; MUID:88067781; PMID:3684607  
A;Accession: A27282  
A;Molecule type: mRNA  
A;Residues: 1-503 <KLE>  
A;Cross-references: UNIPROT:P08103; UNIPARC:UPI0000018DD; GB:Y00487; NID:g51209; PIDN:C,  
R;Holtzman, D.A.; Cook, W.D.; Dunn, A.R.  
Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987  
A;Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed  
A;Reference number: A39973; MUID:88068587; PMID:3317404  
A;Accession: A39973  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-503 <HOL>  
A;Cross-references: UNIPARC:UPI0000018DD; GB:J03023; NID:g192212; PIDN:AAA37305.1; PID:  
C;Genetics:  
A;Gene: hck  
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho  
F;62-110/Domain: SH3 homology <SH3>  
F;121-218/Domain: SH2 homology <SH2>

F;237-495/Region: protein kinase homology <KIN>  
 F;245-253/Region: protein kinase ATP-binding motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted  
 F;267/Active site: Lys #status predicted  
 F;388,499/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	Score	DB	Length
Best Local Similarity	77.8%	1	505
Conservative	66.7%	Pred. No.	33
Mismatches	3	Indels	0
	0	Gaps	0

Qy 1 TFDYLRSQL 9  
 ||||:|||||  
 Db 480 TFEYIQLSVL 488

RESULT 18

TVHUHC  
 protein-tyrosine kinase (EC 2.7.1.112) hck - human  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Dec-1989 #sequence\_revision 10-Nov-1995 #text\_change 05-Oct-2004  
 C;Accession: A27811; A27812; JC1149; C38268; S31103  
 R;Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Diaz, Mol. Cell. Biol. 7, 2267-2275, 1987  
 A;Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and  
 A;Reference number: A27811; MUID:87257942; PMID:3496523  
 A;Accession: A27811  
 A;Molecule type: mRNA  
 A;Residues: 1-505 <QUI>  
 A;Cross-references: UNIPARC:UPI000015C528; GB:M16591  
 A;Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation  
 R;Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmuter, R.M.  
 Mol. Cell. Biol. 7, 2276-2285, 1987  
 A;Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of the  
 A;Reference number: A27812; MUID:87257943; PMID:3453117  
 A;Accession: A27812  
 A;Molecule type: mRNA  
 A;Residues: 1-505 <ZIE>  
 A;Cross-references: UNIPARC:UPI000015C528; GB:M16592; NID:9183913; PID:AA52644.1; PID:  
 R;Hradetzky, D.; Strebsam-Waigmann, H.  
 Gene 113, 275-280, 1992  
 A;Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase  
 A;Reference number: JC1149; MUID:92241680; PMID:1572549  
 A;Accession: JC1149  
 A;Molecule type: DNA  
 A;Residues: 157-505 <HRA>  
 A;Cross-references: UNIPARC:UPI0000172589; EMBL:X59741  
 R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslahti, H.; Alitalo, K.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990  
 A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.  
 A;Reference number: A38268; MUID:91062389; PMID:2247464  
 A;Accession: C38268  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 362-417 <PAR>  
 A;Cross-references: UNIPARC:UPI000017258A  
 C;Genetics:  
 A;Gene: GDB:HCK  
 A;Map position: 20q11-20q12  
 A;Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1  
 C;Function:  
 A;Cross-references: GDB:119303; OMIM:142370  
 A;Map position: 20q11-20q12  
 C;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP  
 C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
 C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phd  
 F;2-505/Product: protein-tyrosine kinase hck #status predicted <MAT>  
 F;64-112/Domain: SH3 homology <SH3>  
 F;123-220/Domain: SH2 homology <SH2>  
 F;239-497/Domain: protein kinase homology <KIN>  
 F;247-255/Region: protein kinase ATP-binding motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted  
 F;269/Active site: Lys #status predicted

F;390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
 Query Match 77.8%; Score 35; DB 1; Length 505;  
 Best Local Similarity 66.7%; Pred. No. 33;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Query Match	Score	DB	Length
Best Local Similarity	75.6%	Score	34
Matches	6	DB	2
	2	Length	211
	1		

Qy 1 TFDYLRSQL 9  
 ||||:|||||  
 Db 526 TFKYLRSQL 534

RESULT 19

H71647  
 alanine-tRNA ligase (EC 6.1.1.7) (alas) RP856 - Rickettsia prowazekii  
 C;Species: Rickettsia prowazekii  
 C;Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
 C;Accession: H71647  
 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.; Nature 396, 133-140, 1998  
 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
 A;Reference number: A71630; MUID:99039499; PMID:9823893  
 A;Accession: H71647  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-877 <AND>  
 A;Cross-references: UNIPROT:Q9ZCA4; UNIPARC:UPI0000136321; GB:AJ235273; GB:AJ235269; NID:91094770  
 A;Experimental source: strain Madrid E  
 C;Genetics:  
 A;Gene: alas; RP856  
 C;Superfamily: alanyl-tRNA ligase  
 C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis  
 Query Match 77.8%; Score 35; DB 2; Length 877;  
 Best Local Similarity 66.7%; Pred. No. 60;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
 ||||:|||||:  
 Db 526 TFKYLRSQL 534

RESULT 20

S12252  
 self incompatibility-associated protein precursor, pistil-specific (allele S2) - Chaco F  
 N;Alternate names: probable ribonuclease S2  
 C;Species: Solanum chacoense (Chaco potato)  
 C;Date: 21-Nov-1993 #sequence\_revision 24-May-1996 #text\_change 31-Dec-2004  
 C;Accession: S12252; S64639  
 R;Xu, B.; Mu, J.; Nevins, D.L.; Grun, P.; Kao, T.  
 Mol. Gen. Genet. 224, 341-346, 1990  
 A;Title: Cloning and sequencing of cDNAs encoding two self-incompatibility associated proteins  
 A;Reference number: S12252; MUID:91094770; PMID:2266940  
 A;Accession: S12252  
 A;Molecule type: mRNA  
 A;Residues: 1-211 <XUB>  
 A;Cross-references: UNIPROT:Q06026; UNIPARC:UPI0000ABEBC; EMBL:X56896; NID:9288518; PID:  
 A;Accession: S64639  
 A;Molecule type: protein  
 A;Residues: 15-29 <XUW>  
 A;Cross-references: UNIPARC:UPI0000175A14  
 C;Superfamily: RNases  
 F;1-14/Domain: signal sequence (fragment) #status predicted <SIG>  
 F;15-211/Product: self incompatibility-associated protein #status experimental <MAT>  
 Query Match 75.6%; Score 34; DB 2; Length 211;  
 Best Local Similarity 66.7%; Pred. No. 21;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
 ||||:|||||:  
 Db 15 TFDYMLKVL 23

RESULT 21  
AC0223 flagellar motor switch protein FlIG [imported] - Yersinia pestis (strain CO92)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AC0223  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A;Title: Genome sequence of *yersinia pestis*, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Accession: AC0223  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-330 <KUR>  
A;Cross-references: UNIPROT:Q8ZF87; UNIPARC:UPI00000DCCE9; GB:AL590842; PIDN:CAC90647.1;  
C;Genetics:  
A;Gene: flIG  
C;Superfamily: flagellar switch protein flIG  
Query Match 75.6%; Score 34; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 DYLRSQL 9  
Db 74 DYLRSQL 80

RESULT 22  
F90963 flagellar motor switch protein FlIG [imported] - Escherichia coli (strain O157:H7, subst  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: F90963  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: F90963  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-331 <HAY>  
A;Cross-references: UNIPROT:P31067; UNIPARC:UPI000012A9AF; GB:BA000007; PIDN:BARB36101.1;  
C;Genetics:  
A;Gene: Ecs2678  
C;Superfamily: flagellar switch protein flIG  
Query Match 75.6%; Score 34; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DYLRSQL 9  
Db 75 DYLRSQL 81

RESULT 23  
H64957 flagellar motor switch protein flIG - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: H64957; JN0905  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of *Escherichia coli* K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: H64957  
A;Status: nucleic acid sequence not shown; translation not shown

RESULT 24  
T03835 vacA protein - slime mold (*Dictyostelium discoideum*) (fragment)  
C;Species: *Dictyostelium discoideum*  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T03835  
R;Shaulsky, G.; Loomis, W.F.  
submitted to the EMBL Data Library, July 1997  
A;Reference number: Z15108  
A;Accession: T03835  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-708 <SHA>  
A;Cross-references: UNIPROT:O15715; UNIPARC:UPI000007945B; EMBL:AF015565; NID:92353180;  
A;Experimental source: train AX4  
C;Genetics:  
A;Gene: vacA

RESULT 25  
G90223 DNA-directed RNA polymerase, subunit F (rpoF) [imported] - *Sulfolobus solfataricus*  
C;Species: *Sulfolobus solfataricus*  
C;Accession: G90223  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Mar-2004  
C;Accession: G90223  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozen, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrest, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: *Sulfolobus solfataricus* complete genome.  
A;Reference number: A99139  
A;Accession: G90223  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-113 <KUR>  
A;Cross-references: UNIPARC:UPI0000066A98; GB:AE006641; NID:g13813918; PIDN:AAK41046.1;

C;Genetics:  
 A;Gene: rpoF  
 C;Superfamily: RNA polymerase, subunit F

Query Match 73.3%; Score 33; DB 2; Length 113;  
 Best Local Similarity 75.0%; Pred. No. 17;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TFDYLRSV 8  
 Db 37 TYDYLNSV 44

RESULT 26

F83703 hypothetical protein BH0430 [imported] - *Bacillus halodurans* (strain C-125)  
 C;Species: *Bacillus halodurans*  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 05-Oct-2004  
 C;Accession: F83703  
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai, N.; Hughes, B.; Huizar, L.  
*Nature* 408, 816-820, 2000  
 C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-223 <STO>  
 A;Cross-references: UNIPROT:Q9KFP8; UNIPARC:UPI00000C3895; GB:AP001508; GB:BA000004; NID:95903043; PIID:1130712

A;Experimental source: strain C-125  
 C;Genetics:  
 A;Gene: BH0430  
 C;Superfamily: Alcaligenes eutrophus phosphoglycolate phosphatase

Query Match 73.3%; Score 33; DB 2; Length 223;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYL 6  
 Db 26 TFDYLR 31

RESULT 27

JH0185 D-amino-acid oxidase (EC 1.4.3.3) - mouse  
 C;Species: *Mus musculus* (house mouse)  
 C;Accession: JH0185  
 R;Tada, M.; Fukui, K.; Momoi, K.; Miyake, Y.  
*Gene* 90, 293-297, 1990  
 A;Title: Cloning and expression of a cDNA encoding mouse kidney D-amino acid oxidase.  
 A;Reference number: JH0185; MUID:90382679; PMID:1976103  
 A;Accession: JH0185  
 A;Molecule type: mRNA  
 A;Residues: 1-345 <TAD>  
 A;Cross-references: UNIPROT:P18894; UNIPARC:UPI000016CE73; GB:M32299; NID:g198571; PIDN:  
 A;Experimental source: kidney, strain BALB/C  
 C;Comment: D-Amino-acid oxidase is a flavoprotein associated with FAD which catalyzes th  
 C;Superfamily: D-amino-acid oxidase  
 C;Keywords: oxidoreductase  
 F;7-12/Domain: FAD binding #status predicted <FAD>  
 F;343-345/Region: peroxisome/glyoxysome location signal (S-[RKH]-L) motif  
 F;54, 209, 215/Active site: Tyr, Lys, His #status predicted

Query Match 73.3%; Score 33; DB 1; Length 345;  
 Best Local Similarity 77.8%; Pred. No. 57;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TFDYLRSVL 9  
 Db 70 TFDYLLSCL 78

RESULT 28

B96567 hypothetical protein F6D8.15 [imported] - *Arabidopsis thaliana* (mouse-ear cress)  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
 C;Accession: B96567  
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.  
*Nature* 408, 816-820, 2000  
 C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-399 <STO>  
 A;Cross-references: UNIPROT:Q9SSR5; UNIPARC:UPI0000AA1FO; GB:AE005173; NID:95903043; PIID:1130712

C;Genetics:  
 A;Gene: F6D8.15  
 A;Map position: 1  
 C;Superfamily: similar to auxin-independent growth promoter (Aux 1)

Query Match 73.3%; Score 33; DB 2; Length 399;  
 Best Local Similarity 75.0%; Pred. No. 67;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FDYLRSVL 9  
 Db 128 FDYIESVL 135

RESULT 29

A40092 protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 16-Jun-2000 #sequence\_revision 16-Jun-2000 #text\_change 05-Oct-2004  
 C;Accession: A40092  
 R;Dymek, S.M.; Niederhuber, J.E.; Desiderio, S.V.  
*Science* 247, 332-336, 1990  
 A;Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.  
 A;Reference number: A40092; MUID:90117147; PMID:2404338  
 A;Accession: A40092  
 A;Molecule type: mRNA  
 A;Residues: 1-499 <DYM>  
 A;Cross-references: UNIPROT:P16277; UNIPARC:UPI000151F18; GB:M30903; NID:g202076; PIDN:  
 A;Gene: MGI:Blk  
 A;Cross-references: MGI:88169  
 A;Map position: 14:28.0  
 C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
 C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho  
 F;59-107/Domain: SH3 homology <SH3>  
 F;118-214/Domain: SH2 homology <SH2>  
 F;233-491/Domain: Protein kinase homology <KIN>  
 F;241-249/Region: protein kinase ATP-binding motif  
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
 F;263/Active site: Lys #status predicted

Query Match 73.3%; Score 33; DB 1; Length 499;  
 Best Local Similarity 66.7%; Pred. No. 84;  
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSVL 9  
 Db 476 TFEFLQSVL 484

RESULT 30

I37206  
protein-tyrosine kinase (EC 2.7.1.112) blk - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 05-Oct-2004  
C;Accession: I37206; S51647  
R;Islam, K.B.; Rabbani, H.; Larsson, C.; Sanders, R.; Smith, C.I.  
J. Immunol. 154, 1265-1272, 1995  
A;Title: Molecular cloning, characterization, and chromosomal localization of a human ly  
A;Reference number: I37206; MUID:95123078; PMID:7822795  
A;Accession: I37206  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-505 <RBS>  
A;Cross-references: UNIPROT:P51451; UNIPARC:UPI0000163B22; EMBL:Z33998; NID:g601951; PID  
C;Genetics:  
A;Gene: GDB:BLK  
A;Cross-references: GDB:454114; OMIM:191305  
A;Map position: 8p23-8p22  
C;Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homology  
C;Keywords: ATP; blocked amino end; Lipoprotein; myristylation; phosphotransferase; tyrd  
F;65-113/Domain: SH3 homology <SH3>  
F;124-220/Domain: SH2 homology <SH2>  
F;239-497/Domain: protein kinase homology <KIN>  
F;247-255/Region: protein kinase ATP-binding motif  
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
F;269/Active site: Lys #status predicted

Query Match 73.3%; Score 33; DB 2; Length 505;  
Best Local Similarity 66.7%; Pred. No. 86;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy	1 TFDYLRSQL	9
	:	
Db	482 TFEFLQSVL	490

Search completed: June 29, 2006, 09:31:35  
Job time : 15.3373 secs

GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on:

June 29, 2006, 08:59:14 ; Search time 97.5904 Seconds

(without alignments)

46.851 Million cell updates/sec

Title: US-10-062-257A-2

Perfect score: 51

Sequence: 1 DYLRSVLEDF 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	51	100.0	10 4	AAG68080
2	51	100.0	10 4	AAB73118
3	51	100.0	10 6	ABR84377
4	51	100.0	10 8	ADS87118
5	51	100.0	10 9	ADX58316
6	51	100.0	10 9	ADZ42231
7	51	100.0	10 9	AEC33133
8	51	100.0	10 10	AEE99214
9	51	100.0	13 4	AAB73144
10	51	100.0	246 4	ABG22263
11	51	100.0	259 2	AYY43955
12	51	100.0	263 8	ADR88385
13	51	100.0	265 7	ABR56203
14	51	100.0	271 7	ABR56204
15	51	100.0	279 9	ADY85449
16	51	100.0	346 3	AYY76750
17	51	100.0	346 4	AAE06208
18	51	100.0	346 5	ABB84435
19	51	100.0	355 8	ABM82980
20	51	100.0	417 2	AAR14201
21	51	100.0	458 7	ADC99048
22	51	100.0	502 5	AAE21689
23	51	100.0	508 3	AB37700

24	51	100.0	508 7	ADE58802
25	51	100.0	508 7	ADE58799
26	51	100.0	508 7	ADF45072
27	51	100.0	508 7	ADL34479
28	51	100.0	508 8	ADS88148
29	51	100.0	509 3	AAY49420
30	51	100.0	509 6	ABR58699
31	51	100.0	509 7	ABR56202
32	51	100.0	509 7	ADE40449
33	51	100.0	509 8	ADL22907
34	51	100.0	509 8	ADP12458
35	51	100.0	509 8	ADP48374
36	51	100.0	509 9	AD251107
37	51	100.0	509 9	AEA35921
38	51	100.0	539 8	ABM82981
39	51	100.0	539 8	ABM82982
40	51	100.0	551 4	ABG22264
41	51	100.0	567 5	ABG79673
42	48	94.1	259 2	AAY43955
43	44	86.3	13 4	AAB73149
44	44	86.3	260 2	AYY43954
45	44	86.3	439 9	ADY52636
46	44	86.3	440 9	ADY52635
47	44	86.3	444 9	ADY52634
48	44	86.3	447 9	ADY52633
49	44	86.3	452 9	ADY52632
50	44	86.3	459 9	ADY52631
51	44	86.3	467 9	ADY52630
52	44	86.3	472 9	ADY52629
53	44	86.3	473 9	ADY52628
54	44	86.3	481 9	ADY52627
55	44	86.3	483 9	ADY52626
56	44	86.3	493 9	ADY52625
57	44	86.3	511 7	ADF45073
58	44	86.3	512 7	ADD19014
59	44	86.3	512 7	ADN95430
60	44	86.3	512 8	ADL22908
61	44	86.3	512 8	ADN04498
62	44	86.3	512 8	ADR14269
63	44	86.3	512 8	ADS88430
64	44	86.3	512 8	ADP23372
65	44	86.3	512 9	ADY16487
66	44	86.3	512 9	ADY19685
67	44	86.3	512 9	ADY14848
68	44	86.3	512 9	ADY52574
69	44	86.3	512 9	AEA35920
70	44	86.3	512 9	AAY29668
71	42	82.4	496 2	AAU08734
72	42	82.4	496 4	AAU08730
73	42	82.4	496 4	Aau08735
74	42	82.4	496 4	Aau08730
75	39	76.5	13 4	AAB73151
76	39	76.5	13 4	Abb73151
77	39	76.5	233 4	Abb71491
78	39	76.5	454 8	Adh48367
79	39	76.5	503 8	Adg97514
80	39	76.5	504 7	Adf45035
81	39	76.5	505 8	ADK70442
82	39	76.5	505 8	ADL22909
83	39	76.5	505 8	ADQ97517
84	39	76.5	505 9	Aea35922
85	39	76.5	558 8	Adr88385
86	38	74.5	13 4	Aab73144
87	38	74.5	13 4	Abg22263
88	38	74.5	13 4	Abg22263
89	38	74.5	13 4	Aay43955
90	38	74.5	13 4	Aay76750
91	38	74.5	17 8	Aee99214
92	38	74.5	272 5	Aab73144
93	38	74.5	279 9	Aab73150
94	38	74.5	279 9	Aay43957
95	38	74.5	316 7	ADJ68978
96	38	74.5	436 8	ADN61468
97	38	74.5	438 9	ADY52642

24	51	100.0	508 7	Ade58802
25	51	100.0	508 7	Ade58799
26	51	100.0	508 7	Adf45072
27	51	100.0	508 7	Adl34479
28	51	100.0	508 8	Ad88148
29	51	100.0	509 3	Aay49420
30	51	100.0	509 6	ABR58699
31	51	100.0	509 7	ABR56202
32	51	100.0	509 7	ADE40449
33	51	100.0	509 8	ADL22907
34	51	100.0	509 8	ADP12458
35	51	100.0	509 8	ADP48374
36	51	100.0	509 9	AD251107
37	51	100.0	509 9	Aea35921
38	51	100.0	539 8	Abm82980
39	51	100.0	539 8	Abm82981
40				



XX  
 PT A detection method of antigen specific T-cells, comprises the use of  
 PT plural antigenic peptides, useful in semi-quantitative determination of  
 PT cancer specific T-cell frequencies and for monitoring cellular immunity.  
 XX  
 PS Example 8; Page 10; 18pp; Japanese.

XX  
 CC The invention relates to a method for the detection of antigen specific T  
 CC -cells in a blood sample involving the use of a plurality of antigenic  
 CC peptides. The method comprises sampling of peripheral blood monocytes;  
 CC stimulation of the collected peripheral blood monocytes with antigens  
 CC without direct use of antigen presenting cells; and detection of T-cells  
 CC specific to the antigen in the stimulated monocytes. The method is  
 CC particularly used for the detection of cancer as it can be used in semi-  
 CC quantitative determination of cancer specific T-cells. It can also be  
 CC used for cancer vaccine therapy for patients with cervical or prostate  
 CC cancer. The method can additionally be used to monitor of cellular  
 CC immunity and cancer immune therapy by detection of specific T-cell  
 CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human  
 CC leukocyte antigen) peptides of human origin used in an example from the  
 CC invention

XX  
 SQ Sequence 10 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	8	10;
Matches	10;	Conservative	Pred. No. 0.021;
	0;	Mismatches	0;
	0;	Indels	0;
	0;	Gaps	0;

Qy 1 DYLRSVLED 10  
 Db 1 DYLRSVLED 10

RESULT 4

ID ADS87118 standard; peptide; 10 AA.

XX  
 AC ADS87118;

XX  
 DT 18-NOV-2004 (first entry)

XX  
 DE Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide 3.

XX  
 KW vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;  
 KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;  
 KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;  
 KW colon; bladder; breast; oesophagus; kidney; brain; human; epitope; Lck.  
 OS Homo sapiens.

XX  
 PN WO2004035085-A1.

XX  
 PD 29-APR-2004.

XX  
 PR 16-OCT-2003; 2003WO-JP013279.

XX  
 PR 17-OCT-2002; 2002JP-00302816.

XX  
 PA (ITOH) ITOH K.

XX  
 PI Itoh K;

XX  
 DR WPI; 2005-152358/16.

PT Prevention and/or therapeutic agent of hematopoietic tumor useful for  
 PT preventing and/or treating hematopoietic tumor, has peptides having amino  
 PT acid sequences of partial peptide of p56lck, SART-1, SART-2, SART-3, or  
 PT ART-1 protein.

XX  
 PS Claim 1; SEQ ID NO 2; 41pp; Japanese.

XX  
 CC The specification describes a remedy for a hematopoietic tumor. The  
 CC remedy comprises one or more peptides derived from p56 (lck), SART-1,  
 CC SART-2, SART-3, or ART-1 proteins as an active ingredient. The peptides  
 CC induce specific cytotoxic T cells. The remedy of the invention is useful  
 PR for preventing and treating hematopoietic tumors comprising human  
 CC leukocyte antigen (HLA)-A24 molecules on its cell surface. It is also  
 CC useful in immunotherapy of hematopoietic tumors, and for treating  
 CC malignant tumors such as acute myelogenous leukemia, acute lymphoblastic  
 CC leukemia, chronic lymphocytic leukemia, malignant lymphoma, multiple  
 CC myeloma, etc. The present sequence represents a partial peptide derived  
 CC from p56, and is used in the remedy of the invention.

XX  
 SQ Sequence 10 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	10;
Matches	10;	Conservative	Pred. No. 0.021;
	0;	Mismatches	0;
	0;	Indels	0;
	0;	Gaps	0;

Qy 1 DYLRSVLED 10  
 Db 1 DYLRSVLED 10

XX  
 CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer  
 CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,  
 CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence  
 CC is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide  
 CC of the invention.

CC Sequence 10 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	8	10;
Matches	10;	Conservative	Pred. No. 0.021;
	0;	Mismatches	0;
	0;	Indels	0;
	0;	Gaps	0;

Qy 1 DYLRSVLED 10  
 Db 1 DYLRSVLED 10

RESULT 5

ID ADX58316 standard; peptide; 10 AA.

XX  
 AC ADX58316;

XX  
 DT 21-APR-2005 (first entry)

XX  
 DE Partial antigenic peptide #2 derived from p56.

XX  
 KW cytostatic; vaccine; hematopoietic tumor; p56; immunotherapy.

XX  
 OS Unidentified.

XX  
 PN WO2005011723-A1.

XX  
 PD 10-FEB-2005.

XX  
 PR 05-AUG-2004; 2004WO-JP011232.

XX  
 PR 05-AUG-2003; 2003JP-00287208.

XX  
 PA (ITOH) ITOH K.

XX  
 PI Itoh K;

XX  
 DR WPI; 2005-152358/16.

PT Prevention and/or therapeutic agent of hematopoietic tumor useful for  
 PT preventing and/or treating hematopoietic tumor, has peptides having amino  
 PT acid sequences of partial peptide of p56lck, SART-1, SART-2, SART-3, or  
 PT ART-1 protein.

XX  
 PS Claim 1; SEQ ID NO 2; 41pp; Japanese.

XX  
 CC The specification describes a remedy for a hematopoietic tumor. The  
 CC remedy comprises one or more peptides derived from p56 (lck), SART-1,  
 CC SART-2, SART-3, or ART-1 proteins as an active ingredient. The peptides  
 CC induce specific cytotoxic T cells. The remedy of the invention is useful  
 PR for preventing and treating hematopoietic tumors comprising human  
 CC leukocyte antigen (HLA)-A24 molecules on its cell surface. It is also  
 CC useful in immunotherapy of hematopoietic tumors, and for treating  
 CC malignant tumors such as acute myelogenous leukemia, acute lymphoblastic  
 CC leukemia, chronic lymphocytic leukemia, malignant lymphoma, multiple  
 CC myeloma, etc. The present sequence represents a partial peptide derived  
 CC from p56, and is used in the remedy of the invention.

XX  
 SQ Sequence 10 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	10;
Matches	10;	Conservative	Pred. No. 0.021;
	0;	Mismatches	0;
	0;	Indels	0;
	0;	Gaps	0;

Qy 1 DYLRSVLED 10  
 Db 1 DYLRSVLED 10

CC Disclosure; SEQ ID NO 134; 266pp; Japanese.

CC The invention relates to a novel genetic vaccine containing the ubiquitin  
 CC gene together with a gene encoding an antigenic protein containing a T-  
 CC cell target sequence. The vaccine of the invention may be useful for  
 prevention and treatment of cancers including melanoma, sarcoma, lymphoma

RESULT 6  
 XX ADZ42231  
 ID ADZ42231 standard; peptide; 10 AA.  
 XX  
 AC ADZ42231;  
 XX DT 30-JUN-2005 (first entry)  
 XX DE Cytotoxic T-lymphocyte epitope peptide, Lck-488.  
 XX KW antibody; vaccine; immune stimulation; cytotoxic T-lymphocyte.  
 XX OS Synthetic.  
 XX PN JP2005099001-A.  
 XX PT 14-APR-2005.  
 XX PF 20-AUG-2004; 2004JP-00240269.  
 PR 31-AUG-2003; 2003JP-00348853.  
 XX PA (UYKA-) UNIV KANAZAWA TECHNOLOGY LICENSING ORG.  
 XX PA Kaneko S, Mizukoshi E, Nakamoto Y, Tsuji H;  
 XX PI DR WPI; 2005-619189/63.  
 XX PT Novel tumor antigen peptide derived from Cyp-B, SART, p53, alpha-fetoprotein and human telomerase reverse transcriptase, useful for preparing anti-tumor peptide vaccine.  
 XX PS Example 1; SEQ ID NO 8; 58PP; Japanese.  
 CC The invention describes a tumor antigen peptide (I) including Cyp-B, SART, p53, multidrug resistance protein (MRP) alpha-fetoprotein (AFP) or human telomerase reverse transcriptase (hTERT) derived peptide comprising an amino acid sequence (S1) of SEQ ID No. 4, 14, 15, 18, 19, 23-25, 27-30, 34, 37-41 or 44. Also described are: an anti-tumor peptide comprising (I); antigen presenting cells (II) presenting (I), obtained by cultivating human leukocyte antigen (HLA)-A24 positive antigen presenting cells with (I); nucleic acid molecule (III) comprising a base sequence encoding (S1); an antibody (A1) capable of specifically binding to (I); inducing (M1) cytotoxic T cells, involves cultivating tumor tissue infiltrated lymphocyte or peripheral blood lymphocyte isolated from the HLA-A24 positive patient, with (I) and interleukin (IL)-2; and anti-tumor agent comprising (II) or the cytotoxic T cell acquired by (M1). (I) is useful for preparing anti-tumor peptide vaccine. The nucleic acid molecule is useful as an anti-tumor agent. The antibody is useful for detecting or diagnosing cancer. (I) is an effective immunogenic peptide with respect to tumor. This is the amino acid sequence of a Lck tumor antigen peptide. Note: This sequence is also available in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).  
 CC SQ Sequence 10 AA;  
 CC Query Match 100.0%; Score 51; DB 9; Length 10;  
 CC Best Local Similarity 100.0%; Pred. No. 0.021;  
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC Qy 1 DYLRSVLED 10  
 CC Db 1 DYLRSVLED 10  
 CC SQ Sequence 10 AA;  
 CC Query Match 100.0%; Score 51; DB 9; Length 10;  
 CC Best Local Similarity 100.0%; Pred. No. 0.021;  
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC Qy 1 DYLRSVLED 10  
 CC Db 1 DYLRSVLED 10  
 RESULT 7  
 AEC33133  
 ID AEC33133 standard; peptide; 10 AA.  
 XX AC AEC33133;  
 XX DT 17-NOV-2005 (first entry)  
 XX DE Lck tumor antigen peptide SEQ ID NO 8.  
 XX KW cytostatic; vaccine; gene therapy; epitope; immunogenicity; diagnosis; tumor-associated antigen; cancer; neoplasm; LCK.  
 KW  
 RESULT 8  
 AEE99214  
 ID AEE99214 standard; peptide; 10 AA.  
 XX AC AEE99214;  
 XX DT 23-FEB-2006 (first entry)  
 XX DE Cancer antigen lck peptide SEQ ID NO 4.  
 XX KW Cytostatic; Vaccine; cancer; neoplasm; antigen; lck.  
 XX OS Unidentified.  
 XX PN WO2005123122-A1.  
 XX PD 29-DEC-2005.  
 XX PF 21-JUN-2005; 2005WO-JP011357.

XX  
PR 21-JUN-2004; 2004JP-00182811.  
XX  
PA (UYKU-) UNIV KURUME.  
XX  
PI Itoh K;  
XX  
DR WPI; 2006-057212/06.  
XX  
PT Treating cancer by evaluating specific cytotoxic T-lymphocyte precursors for each peptide of cancer antigen peptide set, in patient, administering peptide set obtained after removing peptide being non-specific to precursors, to patient.  
XX  
PS Example 1; SEQ ID NO 4; 36pp; Japanese.  
XX  
CC The invention relates to a method of treating a cancer patient by administering cancer antigens to patient, involves evaluating presence or absence of specific cytotoxic T-lymphocyte precursors for individual peptides contained in set of cancer antigen peptides, in patient, removing peptide being non-specific to precursors, from cancer antigen peptide set, to prepare set for administration, and administering cancer antigen peptide set to patient. The method is useful for treating cancer patient by administering cancer antigens to patient. The present sequence represents the amino acid sequence of a lck peptide cancer antigen.  
XX  
SQ Sequence 10 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	4	13;
Matches	10;	Conservative	0;
Mismatches	0;	Indels	0;
Indels	0;	Gaps	0;

Oy 1 DYLRSVLED 10  
Db 3 DYLRSVLED 12

RESULT 10  
ID ABG22263  
ID ABG22263 standard; protein; 246 AA.  
XX  
AC ABG22263;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #22254.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
DN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
XX  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR N-PSDB; AAS86450.  
XX  
WPI; 2001-639362/73.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.  
XX  
PS Claim 20; SEQ ID NO 52622; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
The present invention relates to peptides which are partial sequences of src/Jck family proteins. The present sequence is one such peptide. The peptides are useful for producing vaccines for the treatment of cancer.

SQ Sequence 246 AA;

Query Match 100.0%; Score 51; DB 4; Length 246;

Best Local Similarity 100.0%; Pred. No. 0.6;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLEDF 10

Db 225 DYLRSVLEDF 234

RESULT 11

AC ADR88385;

XX DT 18-NOV-2004 (first entry)

XX DE LCK tyrosine kinase protein.

XX KW Molecular scaffold; nuclear hormone receptor; TNF receptor; G-protein coupled receptor; methyl transferase; ligase;

KW LCK tyrosine kinase; enzyme.

XX OS Unidentified.

XX PN US2004171062-A1.

XX PD 02-SEP-2004.

XX PF 28-FEB-2003; 2003US-00377268.

XX PR 28-FEB-2002; 2002US-0360651P.

PR 16-SEP-2002; 2002US-0411398P.

PR 20-SEP-2002; 2002US-0412341P.

PR 02-JAN-2003; 2003US-0437929P.

XX PA (PLEX-) PLEXXIKON INC.

XX PI Hirth K, Milburn MV;

XX DR WPI; 2004-642017/62.

XX PT Designing a ligand binding to a target molecule, comprises identifying as molecular scaffolds compounds binding to members of a molecular family,

PT detecting orientation of scaffolds at a binding site of target, and

PT synthesizing ligand.

XX PS Disclosure; SEQ ID NO 24; 186pp; English.

XX CC The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the LCK tyrosine kinase protein. This sequence is used to illustrate the method of invention.

CC SQ Sequence 263 AA;

Query Match 100.0%; Score 51; DB 8; Length 263;

Best Local Similarity 100.0%; Pred. No. 0.64;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLEDF 10

Db 250 DYLRSVLEDF 259

RESULT 13

AC ABR56203

ID ABR56203 standard; protein; 265 AA.

XX AC ABR56203;

XX DT 18-DEC-2003 (first entry)

XX DE Mutant Lymphocyte Cell Kinase, Lck, fragment (237-501, D364N).

XX KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;

KW Src-family protein tyrosine kinase; T-cell; immune response; mutant.

XX OS Homo sapiens.

RESULT 12

AC ADR88385

ID ADR88385 standard; protein; 263 AA.

XX

/note= "Phosphorylation site"

OS Synthetic.

XX

FH FT Location/Qualifiers

FT Key /note= "Wild-type D substituted with N. This position is

FT Misc-difference 128 364 in the full-length sequence (see ABR56202 for the

FT wild-type full length sequence"

FT Modified-site 158 /note= "Phosphorylation site"

XX PN WO2003020880-A2.

XX PD 13-MAR-2003.

XX PF 02-AUG-2002; 2002WO-US024546.

XX PR 03-AUG-2001; 2001US-0310051P.

XX PA (ABBO ) ABBOTT LAB.

XX PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;

XX PI Leung A, Ritter K;

XX DR WPI; 2003-300872/29.

XX PT New crystalline polypeptide comprising ligand binding domain or catalytic

PT domain of Lck protein, for determining three-dimensional structure of

PT catalytic domain of Lck, has predetermined unit cell parameters.

XX PS Example 1; Fig 3; 994pp; English.

XX CC The present invention relates to a crystalline polypeptide (I),

CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)

CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily

CC in T-cells and plays an essential role in immune response. (I) is useful

CC for identifying a compound which is an inhibitor of human Lck protein.

XX PS Claim 12; Fig 2; 994pp; English.

XX CC The present invention relates to a crystalline polypeptide (I),

CC comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck)

CC protein. Lck is a Src-family protein tyrosine kinase expressed primarily

CC in T-cells and plays an essential role in immune response. (I) is useful

CC for identifying a compound which is an inhibitor of human Lck protein.

CC The present sequence is a mutated fragment of the human Lck sequence,

CC which approximately comprises the catalytic domain

XX SQ Sequence 271 AA;

Query Match Best Local Similarity 100.0%; Score 51; DB 7; Length 271;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLEDF 10

Db 252 DYLRSVLEDF 261

RESULT 14

ABR56204 ID ABR56204 standard; protein; 271 AA.

XX AC ABR56204;

XX DT 18-DEC-2003 (first entry)

XX DE Mutant Lymphocyte Cell Kinase, Lck, fragment (231-501, D364N).

XX KW Human; protein co-ordinate data; Lymphocyte Cell Kinase; Lck; enzyme;

XX KW Src-family protein tyrosine kinase; T-cell; immune response; mutein;

XX KW mutant.

OS Homo sapiens.

XX OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 134 /note= "Wild-type D substituted with N. This position is

FT 364 in the full-length sequence (see ABR56202 for the

FT wild-type full length sequence"

FT Modified-site 164

FT FT WO2003020880-A2.

FT PN 13-MAR-2003.

FT PD 02-AUG-2002; 2002WO-US024546.

FT PR 03-AUG-2001; 2001US-0310051P.

FT PA (ABBO ) ABBOTT LAB.

FT XX PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hrnciar P, Loew A;

FT XX PI Leung A, Ritter K;

FT XX DR WPI; 2005-273155/28.

FT XX PT New scaffold library used for identifying and developing ligands for

PT protein kinases and treating kinase associated disorders e.g. cancer,  
 PT comprises set of compounds comprising N-heterocyclic compounds.  
 XX Disclosure; Page 170-174; 236pp; English.

CC The invention relates to a new kinase scaffold library comprises at least  
 1 set of compounds, each set comprising at least 1 N-heterocyclic  
 compound of formulae (I) - (VII) given in the specification. Also included  
 are a system for fitting compounds in binding sites of protein kinases  
 (comprising an electronic kinase scaffold, and a scaffold library  
 comprising at least 1 collection of electronic representations of (I)-  
 (VII), where the scaffold library is embedded in a computer device and  
 the electronic representations of the compounds can be selectively  
 retrieved and functionally connected with computer software adapted to  
 fit electronic representations of compounds in an electronic  
 representation of a binding site of a kinase), obtaining improved ligands  
 binding to a protein kinase (which comprises determining if a derivative  
 of (I) - (VII) binds to the kinase with greater affinity and/or specificity  
 than (I) - (VII)), developing ligands specific for a particular kinase  
 (which comprises determining if a derivative of (I) - (VII) that binds to  
 kinases has greater for specificity for the particular kinase than (I)-  
 (VII), developing ligands binding to a kinase (which comprises  
 determining the orientation of at least 1 molecular scaffold of (I) - (VII)  
 in co-crystals with the kinase, identifying chemical structures of the  
 which at least 1 chemical structure of the scaffold is modified),  
 developing ligands with increased specificity on a kinase (which  
 comprises testing a derivative of a kinase binding compound (I) - (VII) for  
 increased specificity on the kinase), identifying a ligand binding to a  
 kinase (which comprises determining if a derivative compound including a  
 core structure (I) - (VII) binds to the kinase with changed binding  
 affinity and/or specificity), a co-crystal of a kinase and a binding  
 compound (I) - (VII), preparation of co-crystals of Pim-1 with (I) - (VII),  
 CC identifying potential kinase binding compounds (which comprises fitting  
 electronic representations of (I) - (VII) in an electronic representation  
 of a kinase binding site), attaching a kinase binding compound to an  
 attachment component (which comprises identifying energetically allowed  
 sites for attachment of the component on a kinase binding compound (I) -  
 (VII) and attaching the compound or derivative to the attachment  
 component at the allowed site), modified compounds (comprising (I) - (VIII))  
 CC with an attached linker group, and developing a ligand for a kinase  
 comprising conserved residues matching at least one of Pim-1 residues 49,  
 52, 67, 121, 128 and 186 which comprises determining if (I) - (VII) binds  
 to the kinase. The kinases comprise Pim-1, Pyk2, c-Abl, Her2, cMet,  
 vascular endothelial growth factor receptor, endothelial growth factor  
 receptor, ckit, Pkcbeta, p38, Cdk2, Akt or Gsk3beta. The kinase scaffold  
 CC represents a continuous amino acid sequence.  
 CC sequence 279 AA;

Query Match 100.0%; Score 51; DB 9; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 0.69;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLEDF 10  
 Db 258 DYLRSVLEDF 267

RESULT 16  
 AAY76750 standard; protein; 346 AA.  
 ID AAY76750  
 XX

AC AAY76750;  
 XX DT 17-APR-2000 (first entry)  
 XX DE Human protein kinase homologue, PKH-3.  
 XX KW Protein kinase homologue; human; PKH; diagnosis; therapy; cancer; AIDS;  
 CC autoimmune disorder; inflammatory disorder; reproductive defect; asthma;  
 CC diabetes mellitus; infertility; ovulatory defect; endometriosis;  
 CC polycystic ovary syndrome.  
 XX OS Homo sapiens.  
 XX PN US6013455-A.  
 XX PD 11-JAN-2000.  
 XX PF 15-OCT-1998; 98US-00173581.  
 XX PR 15-OCT-1998; 98US-00173581.  
 XX PA (INCY-) INCYTE PHARM INC.  
 XX PI Hillman JL, Yue H, Yang YT, Corley NC, Gorgone GA, Azimzai Y;  
 DR Lu DAM, Bandman O, Guegler KJ;  
 XX WPI; 2000-136321/12.  
 DR N-PSDB; AAZ86794.

XX PS Nucleic acids encoding a human protein kinase homolog useful for  
 PT preventing, diagnosing and treating cancer, autoimmune/inflammatory  
 PT disorders and reproductive defects.

XX PS Claim 1; Col 47-50; 38pp; English.

CC This sequence represents a human protein kinase homolog (PKH) of the  
 CC invention. The PKH sequences may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate PKH expression such  
 CC as cancers, autoimmune/inflammatory disorders and reproductive defects.  
 CC They may be used to treat disorders associated with decreased PKH  
 CC expression such as cancers (e.g. lymphoma, melanoma and cancers of the  
 CC breast lung and prostate), autoimmune/inflammatory disorders (e.g. AIDS,  
 CC asthma and diabetes mellitus), and reproductive defects (e.g.  
 CC infertility, ovulatory defects, endometriosis and polycystic ovary  
 CC syndrome). The DNA may be administered to treat diseases by rectifying  
 CC mutations or deletions in a patient's genome that affect the activity of  
 CC PKH by expressing inactive proteins or to supplement the patient's own  
 CC production of PKH polypeptides. Additionally, the DNA may be used to  
 CC produce PKH, according to standard recombinant DNA methodology, by  
 CC inserting the nucleic acids into a host cell and culturing the cell to  
 CC express the protein. Conversely, antisense nucleic acid molecules may be  
 CC administered to down regulate PKH expression by binding with the cells  
 CC own PKH genes and preventing their expression. The DNA, and antisense  
 CC sequences may also be used as DNA probes in diagnostic assays to detect  
 CC and quantitate the presence of similar nucleic acid sequences in samples,  
 CC and hence which patients may be in need of restorative therapy. They may  
 CC also be used to study the expression and function of PKH polypeptides and  
 CC their role in metabolism. The PKH polypeptides may be used as antigens in  
 CC the production of antibodies against PKH and in assays to identify  
 CC modulators (agonists and antagonists) of PKH expression and activity. The  
 CC anti-PKH antibodies and PKH antagonists may also be used to down regulate  
 CC PKH expression and activity. The anti-PKH antibodies may also be used as  
 CC diagnostic agents for detecting the presence of PKH polypeptides in  
 CC samples

XX SQ Sequence 346 AA;

Query Match 100.0%; Score 51; DB 3; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 0.86;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLEDF 10  
 XX



CC respiratory distress syndrome, allergies, ankylosing spondylitis,  
 CC amyloidosis, anaemia, asthma, atherosclerosis, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, bronchitis, cholecystitis, cancer,  
 CC contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis,  
 CC diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis,  
 CC Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis,  
 CC hypereosinophilia, irritable bowel syndrome, multiple sclerosis,  
 CC myasthenia gravis, myocardial or pericardial inflammation,  
 CC osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis,  
 CC Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjogren's syndrome,  
 CC systemic lupus erythematosus (SLE), systemic sclerosis, thrombocytopenic  
 CC purpura, ulcerative colitis, uveitis, Werner syndrome, complications of  
 CC cancer, haemodialysis, and extracorporeal circulation, viral, bacterial,  
 CC fungal, parasitic, protozoal, and helminthic infections, infertility,  
 CC including tubal disease, ovulatory defects, and endometriosis,  
 CC disruptions of the oestrous cycle, disruptions of the menstrual cycle,  
 CC polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial  
 CC and ovarian tumours, uterine fibroids, autoimmune disorders, ectopic  
 CC pregnancies, and teratogenesis. The polypeptides of the invention can be  
 CC used for gene therapy. This sequence represents a PKH from clone ID  
 CC 507669 isolated from TMLR3DPT02, a library constructed using RNA isolated  
 CC from non-adherent peripheral blood mononuclear cells collected from a  
 CC pool of male and female donors  
 XX

SQ Sequence 346 AA;

Query	Match	Score	DB	Length
Best Local Similarity	100.0%	51	5	346
Matches	10; Conservative	0	Mismatches	0; Indels
Qy	1 DYLRSVLED <span style="background-color: yellow;">F</span>	10		
Db	325 DYLRSVLED <span style="background-color: yellow;">F</span>	334		

RESULT 19

ABM82980 Query Match 100.0%; Score 51; DB 5; Length 346;

ID ABM82980 Best Local Similarity 100.0%; Pred. No. 0.86; Mismatches 0; Indels 0; Gaps 0;

XX AC ABM82980; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:3229.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
 OS Homo sapiens.  
 XX WO2004023973-A2.  
 XX PD 25-MAR-2004.  
 XX PR 12-SEP-2003; 2003WO-US028227.  
 XX PR 12-SEP-2002; 2002US-0410259P.  
 XX PA (INCYT-) INCYTE CORP.  
 XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
 PI Hartshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
 PI Mooney EM, Deleageane AM, Panesar IS, Banville SC, Reddy TP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patury S, Shi X, Suarez CJ;  
 XX DR WPI; 2004-329368/30.  
 XX DR N-PSDB; ACN41632.

PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 PS Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

SQ Sequence 355 AA;

Query	Match	Score	DB	Length
Best Local Similarity	100.0%	51	8	355
Matches	10; Conservative	0	Mismatches	0; Indels
Qy	1 DYLRSVLED <span style="background-color: yellow;">F</span>	10		
Db	334 DYLRSVLED <span style="background-color: yellow;">F</span>	343		

RESULT 20

AAR14201 Query Match 100.0%; Score 51; DB 8; Length 355;

ID AAR14201 Best Local Similarity 100.0%; Pred. No. 0.88; Mismatches 0; Indels 0; Gaps 0;

XX AC AAR14201; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DT 13-DEC-1991 (first entry)

DE (Beta-galactosidase N-terminal) - (lck gene prod.) fusion protein.

KW Multi-cloning site.

OS Synthetic.

XX FH Key Location/Qualifiers

FT Region 1..26 /note= "beta-galactosidase fragment"

FT Region 27..417 /note= "lck gene polypeptide"

FT JP03201994-A.

PN 03-SEP-1991.

XX PD 28-DEC-1989; 89JP-00338268.

XX PR 28-DEC-1989; 89JP-00338268.

XX PA (TOKU) TOKUYAMA SODA KK.

XX DR WPI; 1991-300980/41.

DR N-PSDB; AAQ14201.

PT Fused polypeptide - has amino acid sequence of beta-galactosidase with a

PT LCK gene conjugated to the N-terminal via DNA having multi-cloning site.

XX PS Claim 1; Fig 4,2; 15pp; Japanese.

XX CC The sequence consists of the N-terminal amino acids of the beta-

New diagnostic and therapeutic polynucleotides and polypeptides, useful

CC galactosidase gene fused with the lck gene. It is produced by E.coli  
 CC transformed with a recombinant vector (see AAQ13983). It is useful for  
 CC producing an antibody specifically immunoreactive with only a lck gene-  
 CC derived polypeptide in T cells. The antibody may recognise lck gene-  
 XX Sequence 417 AA;

Query Match 100.0%; Score 51; DB 2; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 1;  
 Matches 10; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;  
 Qy 1 DYLRSVLED 10  
 Db 396 DYLRSVLED 405

SQ Sequence 417 AA;

RESULT 21  
 ADC99048 ID ADC99048 standard; protein; 458 AA.

XX AC ADC99048;  
 XX DT 01-JAN-2004 (first entry)

XX DE Human KPP protein - SEQ ID 1.

XX KW anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian;  
 KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;  
 KW immunosuppressive; antithyroid; cytostatic; hepatotrophic; dermatological;  
 KW antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;  
 KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic;  
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;  
 KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;  
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;  
 KW cancer; developmental; mental retardation; neurological;  
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory;  
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;  
 KW helminthic infection; transgenic; gene therapy; human; enzyme.  
 XX OS Homo sapiens.

XX PN WO2003033680-A2.

XX PD 24-APR-2003.

XX PF 17-OCT-2002; 2002WO-US033723.

XX PR 19-OCT-2001; 2001US-0345474P.

XX PR 02-NOV-2001; 2001US-0343910P.

XX PR 13-NOV-2001; 2001US-0333098P.

XX PR 16-NOV-2001; 2001US-0332424P.

XX PR 30-NOV-2001; 2001US-0334288P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;

PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvard AE, Griffin JA;

PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;

PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;

PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;

PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;

XX PA Zebarjadian Y;

XX DR WPI; 2003-403214/38.

XX DR N-PSDB; ADC99100.

XX New human kinases and phosphatases and polynucleotides, useful for  
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders  
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,  
 PT cancer or hepatitis.

XX Claim 1; SEQ ID NO 1; 424pp; English.

XX The invention relates to a novel isolated polypeptide which is a human  
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,  
 CC agonists and antagonists are useful for diagnosing, treating or  
 CC preventing cell proliferative disorders such as atherosclerosis,  
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental  
 CC retardation, neurological disorders including Alzheimer's disease and  
 CC Parkinson's disease, autoimmune and inflammatory disorders such as  
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the  
 CC polynucleotides encoding KPP may be useful for creating transgenic  
 CC animals to model human disease, as well as during gene therapy  
 CC procedures. The current sequence is that of the human KPP protein of the  
 CC invention.

SQ Sequence 458 AA;

RESULT 22  
 AAE21689 ID AAE21689 standard; protein; 502 AA.

XX AC AAE21689;  
 XX DT 29-AUG-2003 (revised)  
 XX DT 16-JUL-2002 (first entry)

DE Fugu rubripes Lymphocyte kinase (LCK) protein.

XX KW T-Lymphocyte modulator; autoimmune disorder; graft rejection;  
 KW graft-versus-host disease; viral infection; Lymphocyte kinase; LCK.

XX OS Takifugu rubripes.

XX PN WO200218619-A2.

XX PD 07-MAR-2002.

XX PF 16-AUG-2001; 2001WO-11000765.

XX PR 01-SEP-2000; 2000US-0229326P.

XX PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
 PA (EHRL-) EHRLICH G.

XX PI Brenner S, Venkatesh B, Tan YH;

XX DR WPI; 2002-329781/36.

XX DR N-PSDB; AAD34173.

XX New nucleic acids, useful for regulating T-cell mediated immune  
 PT responses, e.g., suppressing T-lymphocytes in subjects with autoimmune  
 PT disorders, or enhancement in those with viral infections, comprises novel  
 PT T-cell active promoters.

XX PS Example 2; Page 55-57; 67pp; English.

XX The invention relates to an isolated nucleic acid which includes a  
 CC promoter sequence being transcriptionally functional in a T-lymphocyte  
 CC undergoing activation and transcriptionally less functional in the T-  
 CC lymphocyte prior to the activation. The nucleic acid is useful for  
 CC regulating T-cell mediated immune responses in mammals. Nucleic acid  
 CC molecules of the invention may be used to suppress or eliminate T-  
 CC lymphocytes undergoing activation to suppress T-lymphocyte mediated  
 immune response in individuals suffering from immune disorders, e.g.



Query Match 100.0%; Score 51; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Sequence 508 AA;

Qy 1 DYLRSVLED 10  
 Db 487 DYLRSVLED 496

RESULT 25

Query Match 100.0%; Score 51; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Sequence 508 AA;

Qy 1 DYLRSVLED 10  
 Db 487 DYLRSVLED 496

ADE58799  
 ID ADE58799 standard; protein; 508 AA.  
 XX  
 AC ADE58799;  
 XX  
 DT 29-JAN-2004 (first entry)  
 DE Human Protein P06239, SEQ ID NO 4686.  
 XX  
 KW Human; pain; neuronal tissue; gene therapy;  
 spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.

XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.

XX  
 PI Woolf C, Durso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.

XX  
 PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.

XX  
 CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Query Match 100.0%; Score 51; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Sequence 508 AA;

Qy 1 DYLRSVLED 10  
 Db 487 DYLRSVLED 496

RESULT 26

Query Match 100.0%; Score 51; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Sequence 508 AA;

Qy 1 DYLRSVLED 10  
 Db 487 DYLRSVLED 496

ADF45072  
 ID ADF45072 standard; protein; 508 AA.  
 XX  
 AC ADF45072;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human kinase LCK.  
 XX  
 KW Human; protein kinase; enzyme; inhibitor; LCK.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003081210-A2.  
 XX  
 PD 02-OCT-2003.  
 XX  
 PF 20-MAR-2003; 2003WO-US008725.  
 XX  
 PR 21-MAR-2002; 2002US-0366892P.  
 XX  
 PA (SUNE-) SUNESIS PHARM INC.  
 XX  
 PI Prescott JC, Braisted A;  
 XX  
 DR WPI; 2003-865136/80.

PT Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T') which contains reactive group at binding site, with ligands and detecting PT kinase-ligand conjugate formation.

XX  
 PS Disclosure; SEQ ID NO 41; 260pp; English.

CC The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T'), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.

CC  
 XX  
 SQ Sequence 508 AA;

Query Match 100.0%; Score 51; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Sequence 508 AA;

Qy 1 DYLRSVLED 10  
 Db 487 DYLRSVLED 496

RESULT 27

ADL3479

ID ADL34479 standard; peptide; 508 AA.  
 XX  
 AC ADL34479;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human lymphocyte kinase (Lck) globular core.  
 XX  
 KW cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;  
 KW fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;  
 KW protein-ligand complex; lymphocyte kinase; Lck; Lck ligand;  
 KW kinase inhibitor; therapeutic; kinase-mediated physiological event;  
 KW cancer; autoimmunological; metabolic; inflammatory; infection;  
 KW central nervous system degenerative disease; transplant rejection; human;  
 KW globular core; protein co-ordinate data.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6589758-B1.  
 XX  
 PD 08-JUL-2003.  
 XX  
 PF 21-MAY-2001; 2001US-00862154.  
 XX  
 PR 19-MAY-2000; 2000US-0205510P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Zhu X;  
 XX  
 DR WPI; 2003-810380/76.  
 XX  
 PT Crystal of protein-ligand complex useful for identifying an inhibitor of  
 PT lymphocyte kinase (Lck), comprises truncated Lck and a ligand.  
 PS Claim 1; SEQ ID NO 1; 295pp; English.  
 XX  
 CC The invention describes a crystal (I) of a protein-ligand complex (C)  
 CC comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I)  
 CC effectively diffracts X-rays for determination of atomic coordinates of  
 CC (C) to a resolution of greater than 5.0 angstroms, and truncated Lck  
 CC comprises a sequence (S1) of residues 225-508 of a 508 amino acid  
 CC sequence, given in specification and retains the globular core of full-  
 CC length Lck. (I) is useful in an inhibitor screening assay and to  
 CC identify, design, select, and evaluate potential inhibitors of kinases  
 CC that would be useful as therapeutics for diseases or symptoms of diseases  
 CC that are associated with kinase-mediated physiological events. The  
 CC inhibitors identified by the methods may also be useful for inhibition of  
 CC kinase activity of one or more enzymes. The inhibitors are also useful  
 CC for inhibiting the biological activity of any enzyme comprising greater  
 CC than 90%, alternatively greater than 85%, or alternatively greater than  
 CC 70% sequence homology with a kinase sequence. The inhibitors are useful  
 CC for inhibiting the biological activity of any enzyme that binds ATP and  
 CC thus for treating disease or disease symptoms mediated by any enzyme that  
 CC binds ATP. The inhibitors are useful in inhibiting kinase activity and  
 CC are useful in treating kinase-mediated disease or disease symptoms in a  
 CC mammal, particularly a human e.g., cancer, autoimmunological, metabolic,  
 CC inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central  
 CC nervous system degenerative disease etc. The inhibitors are useful in  
 CC treating or preventing diseases, including, transplant rejection etc.  
 CC This is the amino acid sequence of a human lymphocyte kinase (Lck)  
 CC polypeptide comprising the Lck globular core.  
 XX  
 SQ Sequence 508 AA;

Query Match 100.0%; Score 51; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLED 10  
 ||||| |||||  
 Db 487 DYLRSVLED 496

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RESULT 28  
 ID ADS8148  
 ID ADS8148 standard; protein; 508 AA.  
 XX  
 AC ADS8148;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human protein of a TNF-alpha signalling pathway protein complex seqID 3.  
 XX  
 KW protein complex; tumour necrosis factor-alpha signalling pathway;  
 KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;  
 KW inflammatory bowel disease; infectious disease; septic shock;  
 KW bacterial infection; neurological disease; stroke-induced inflammation;  
 KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;  
 KW antirheumatic; cytostatic; antibacterial; gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004035783-A2.  
 XX  
 PD 29-APR-2004.  
 XX  
 PR 24-SEP-2003; 2003WO-EP050655.  
 XX  
 PR 26-SEP-2002; 2002EP-00021809.  
 PR 10-FEB-2003; 2003EP-00100274.  
 XX  
 PA (CELL-) CELLZONE AG.  
 XX  
 PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;  
 PI Superti-Furga G, Kruse U;  
 DR WPI; 2004-348460/32.  
 XX  
 PT New protein complex comprising at least one first and second protein of  
 PT the tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for  
 PT diagnosing or treating inflammation, neurological diseases, infectious  
 PT diseases or cancer.  
 XX  
 PS Example; SEQ ID NO 3; 1980pp; English.  
 XX  
 CC This invention relates to novel protein complexes of the tumour necrosis  
 CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to  
 CC methods for preparing these complexes comprising at least two component  
 CC proteins, as well as screening methods to identify modulators of the  
 CC pathway, which include antibodies, agonists and antagonists thereof. The  
 CC present invention describes a protein complex and kit that are useful for  
 CC diagnosing, prognosing or treating chronic inflammatory diseases such as  
 CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases  
 CC such as septic shock and bacterial infections; neurological diseases such  
 CC as stroke-induced inflammation in neurons; neurodegenerative diseases and  
 CC cancer. Accordingly, these complexes can be used for the development of  
 CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,  
 CC antirheumatic, cytostatic and antibacterial activities and can be used  
 CC for gene therapy purposes. In particular, the invention further provides  
 CC siRNA-oligonucleotides useful for inhibiting protein expression for in  
 CC vitro or cell culture assays. This polypeptide is a human protein that  
 CC can be used in combination with other proteins provided in the  
 CC specification to form novel complexes of the TNF-alpha signalling pathway  
 CC of the invention.  
 XX  
 SQ Sequence 508 AA;

Query Match 100.0%; Score 51; DB 8; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLED 10  
 ||||| |||||  
 Db 487 DYLRSVLED 496

**RESULT 29**  
**XX AC AAY49420;**  
**ID AAY49420 standard; protein; 509 AA.**  
**XX XX DT AAY49420;**  
**XX DE 13-MAR-2000 (first entry)**  
**PKA substrate, Src-family protein.**  
**KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;**  
**KW kinase substrate; immunosuppressive disorder; proliferative disease;**  
**KW HIV infection; AIDS; immunodeficiency; autoimmune disease;**  
**KW systemic Lupus erythematosus; Src-family.**  
**XX OS Homo sapiens.**  
**XX PN WO9962315-A2.**  
**XX PD 02-DEC-1999.**  
**XX PR 27-MAY-1999; 99WO-GB001680.**  
**XX PR 27-MAY-1998; 98NO-00002419.**  
**XX PR 30-DEC-1998; 98US-0114240P.**  
**XX PA (LAUR-) LAURAS AS.**  
**PA (JONE/) JONES E L.**  
**XX PI Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V;**  
**PI Tasken K, Vang T, Altman A, Munshi A;**  
**XX DR N-PSDB; AAZ46491.**  
**XX PT Altering the activity of protein kinase signaling pathways, used for**  
**PT treating immunosuppressive disorders, e.g. AIDS, proliferative disorders,**  
**PT e.g. cancers or autoimmune diseases.**  
**XX PS Claim 23; Page 95-96; 111pp; English.**  
**XX CC The invention provides a novel method of altering the activity of the**  
**CC protein kinase A (PKA) signaling pathway in a cell that comprises**  
**CC altering the extent of phosphorylation of one or more PKA substrates, or**  
**CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical**  
**CC compositions containing a nucleic acid molecule that encodes a PKA**  
**CC substrate, or fragment, precursor or functionally equivalent variant,**  
**CC where the sequence is modified to alter its susceptibility to**  
**CC phosphorylation by PKA can be used for treating a disorder exhibiting**  
**CC abnormal PKA signaling activity, immunosuppressive disorders or**  
**CC proliferative diseases. They can be used for treating e.g. HIV infection,**  
**CC AIDS, common variable immunodeficiency or cancers. Conditions in which**  
**CC upregulation of the PKA pathway is required, such as autoimmune disease,**  
**CC e.g. systemic Lupus erythematosus, may also be treated. The present**  
**CC sequence represents a PKA substrate, wherein the substrate is in the Src-**  
**CC family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-tyk,**  
**CC Fyk, Src-1 or Src-2**  
**XX Sequence 509 AA;**

---

**XX AC ABR58699;**  
**XX XX DT 09-JUL-2003 (first entry)**  
**DE Human cancer related protein SEQ ID NO:356.**  
**KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;**  
**KW heart disease; atherosclerosis; endometriosis.**  
**XX OS Homo sapiens.**  
**XX PN WO2003025138-A2.**  
**XX PD 27-MAR-2003.**  
**XX PR 17-SEP-2002; 2002WO-US029560.**  
**XX PR 17-SEP-2001; 2001US-0323469P.**  
**PR 20-SEP-2001; 2001US-0323887P.**  
**PR 13-NOV-2001; 2001US-0350666P.**  
**PR 08-FEB-2002; 2002US-0355145P.**  
**PR 08-FEB-2002; 2002US-0355257P.**  
**PR 12-APR-2002; 2002US-0372246P.**  
**XX PA (EOSB-) EOS BIOTECHNOLOGY INC.**  
**XX PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;**  
**PI Zlotnik A;**  
**XX DR N-PSDB; ACC72850.**  
**XX PT New genes that are up-regulated or down-regulated in cancers, useful as**  
**PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as**  
**PT therapeutic targets for screening drugs for treating these diseases.**  
**XX PS Claim 12; Page 762; 767pp; English.**  
**XX CC The present invention describes an isolated nucleic acid molecule, which**  
**CC comprises the sequence of any of the genes that are up-regulated or down-**  
**CC regulated in specific cancers (e.g. about 1031 genes up-regulated in**  
**CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer**  
**CC related gene nucleotide sequences which encode the proteins given in**  
**CC ABR58521 to ABR58709. Also described: (1) determining the presence or**  
**CC absence of a pathological cell in a patient; (2) an expression vector**  
**CC comprising a nucleic acid molecule described above; (3) a host cell**  
**CC comprising the vector; (4) an isolated polypeptide, which is encoded by**  
**CC the nucleic acid; (5) an antibody that specifically binds the polypeptide**  
**CC of (4); (6) specifically targeting a compound to a pathological cell in a**  
**CC patient by administering to the patient the antibody above; and (7) a**  
**CC drug screening assay. The nucleic acid is useful as diagnostic markers or**  
**CC therapeutic targets. In particular, the nucleic acid is useful for**  
**CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,**  
**CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,**  
**CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,**  
**CC atherosclerosis and endometriosis. The nucleic acid is also useful in**  
**CC drug screening, particularly for identifying agents for treating these**  
**CC pathologies**

RESULT 30  
ABR58699  
ID ABR58699 standard; protein; 509 AA.

Search completed: June 29, 2006, 09:13:12  
Job time : 98:5904 secs

Mon Jul 3 08:56:44 2006

us-10-062-257a-2.rag

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GenCore version 5.1.9

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 Seconds  
 (without alignments)  
 78.664 Million cell updates/sec

Title: US-10-062-257A-1  
 Perfect score: 45  
 Sequence: 1 TFDYIERSVL 9

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : UniProt\_7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	45	100.0	368	2 Q3TLX4_MOUSE	Q3tlx4 mus musculu
2	45	100.0	379	2 Q4FZR6_RAT	Q4fzr6 rattus norv
3	45	100.0	502	2 Q8QGJ9_FUGRU	Q8qgj9 fugu rubrip
4	45	100.0	508	1 LCK_AOTNA	Q5pxs1 aotus nancy
5	45	100.0	508	1 LCK_HUMAN	P06239 homo sapien
6	45	100.0	508	1 LCK_MOUSE	P06240 mus musculu
7	45	100.0	508	1 LCK_SAISC	Q95kr7 saimiri sci
8	45	100.0	509	2 Q7RTZ3_HUMAN	Q7rtz3 homo sapien
9	45	100.0	509	2 Q95M32_9PRIM	Q95m32 hylobates s
10	45	100.0	509	2 Q3ZCM0_BOVIN	Q3zcm0 bos taurus
11	45	100.0	516	2 Q573B4_HUMAN	Q573b4 homo sapien
12	42	93.3	249	2 Q9U8V6_SEPTBU	Q9u8v6 eptatretus
13	41	91.1	318	2 Q2UQK7_ASPOR	Q2uqk7 aspergillus
14	41	91.1	466	2 Q4RNX3_TETNG	Q4rnx3 tetraodon n
15	41	91.1	488	2 Q13064_XENLA	Q13064 xenopus lae
16	41	91.1	491	2 Q3U6Q5_MOUSE	Q3u6q5 mus musculu
17	41	91.1	491	2 Q8CE10_MOUSE	Q8ce10 mus musculu
18	41	91.1	492	2 Q5ZMB9_CHICK	Q5zmb9 gallus gall
19	41	91.1	511	1 LYN_HUMAN	P07948 homo sapien
20	41	91.1	511	1 LYN_MOUSE	P25911 mus musculu
21	41	91.1	511	1 LYN_RAT	Q07014 rattus norv
22	41	91.1	512	2 Q3TCS3_MOUSE	Q3tcs3 m nod-deriv
23	41	91.1	582	2 Q6NUK7_HUMAN	Q6nuk7 homo sapien
24	39	86.7	510	2 Q66I04_BRARE	Q66i04 brachydanio
25	38	84.4	605	2 Q4X0L1_ASPPFU	Q4x0l1 aspergillus
26	38	84.4	606	2 Q5AZN3_EMENT	Q5azn3 aspergillus
27	37	82.2	98	2 Q86TW9_HUMAN	Q86tw9 homo sapien
28	37	82.2	267	2 Q5FWT4_RAT	Q8ymut7_anasp
29	37	82.2	379	2 Q3MBB4_ANAVT	Q3mbb4 anabaena va
30	37	82.2	381	2 Q8J1E4_LIPKO	Q8j1e4 lipomyces k

ALIGNMENTS

Q9ddk6	salmo salar
Q6tpq4	brachydanio
P17713	hydra attenuata
Q80y28	mus musculus
Q5nq10	zymomonas nigrifrons
O14678	homo sapiens
Q6iaq0	homo sapiens
Q96e75	homo sapiens
Q39548	cucurbita maxima
Q8ccao	mus musculus
Q2ydw5	mus musculus
Q8c5x2	mus musculus
Q9pj12	chlamydia trachomatis
Q84562	chlamydia trachomatis
Q3kld9	chlamydia trachomatis
Q40nj1	desulfurobacter
O93411	xenopus laevis
P42683	gallus gallus
Q7sg70	neurospora crassa
Q4iqel	gibberella zea mays
O15791	plasmodium
Q8ibz6	plasmodium
Q15801	plasmodium
Q15792	plasmodium
Q581m5	cyanophage
Q5bt64	schistosoma mansoni
Q4xnk1	plasmodium
Q4jb12	sulfolobus
Q5ffy4	ehrlichia rickettsiae
Q5han1	caenorhabditis elegans
O61j95	caenorhabditis elegans
Q9xvx5	caenorhabditis elegans
Q86d99	caenorhabditis elegans
Q5rhx5	brachydanius
Q5rxh6	brachydanius
Q4rkv7	tetraodon nigroviridis
Q55xn5	cryptococcus neoformans
Q5kmal	cryptococcus neoformans
Q7rlie3	plasmodium
Q8ij81	plasmodium
P50545	rattus norvegicus
Q95m30	macaca fasciata
Q3ud17	m. bone marrow
Q6ayv7	rattus norvegicus
Q4rl31	tetraodon nigroviridis
P08103	mus musculus
P08631	homo sapiens
Q76ip5	candida glabrata
Q504rs	homo sapiens
Q2vpe2	homo sapiens
Q44pn7	chlorobium
Q9frx5	cucumis sativus
Q9zca4	rickettsia
Q54hc2	dictyostelia
Q5byf7	schistosoma
Q8fkp1	escherichia coli
Q4imk6	gibberella zea mays
Q06026	solanum tuberosum
Q836y8	enterococcus faecalis
P95715	shigella boydii
Q31rt6	synechococcus
Q5n2ho	synechococcus
Q2jyg3	rhizobium etiopae
Q92564	homo sapiens
Q4v4y8	drosophila melanogaster
Q5wYx0	legionella pneumophila
Q5x7h4	legionella pneumophila
Q5zy00	legionella pneumophila

RESULT 1	
ID	Q3TLX4_MOUSE
AC	Q3TLX4_MOUSE
DT	11-OCT-2005, integrated into UniProtKB/TREMBL.
DT	07-FEB-2006, entry version 7.
DE	Mammary gland RCB-0526 JY9-MC(A) cDNA, RIKEN full-length enriched library, clone:G830026006 product:lymphocyte protein tyrosine kinase, full insert sequence. (Fragment).
GN	Name=Lck;
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
OC	NCBI_TAXID=10090;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Mammary gland;
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J., Jarvis E.D., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Konagaya A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
RA	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RT	Nature 420:563-573 (2002).
RL	[5]
RN	RP
RC	NUCLEOTIDE SEQUENCE.
RX	TISSUE=Mammary gland;
RA	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
RA	"Functional annotation of a full-length mouse cDNA collection.";
RT	Nature 409:685-690 (2001).
RL	[6]
RN	RP
RC	NUCLEOTIDE SEQUENCE.
RX	TISSUE=Mammary gland;
RA	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RT	Genome Res. 10:1617-1630(2000).
RL	[7]
RN	RP
RC	NUCLEOTIDE SEQUENCE.
RX	TISSUE=Mammary gland;
RG	PubMed=16141073; DOI=10.1126/science.1112009;
RG	RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
RG	"The transcriptional landscape of the mammalian genome.";
RG	Science 309:1559-1563 (2005).
RN	[3]

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuurra S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 [8]

RN  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shevchenko C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnarch A., Schein J.B., Jones S.J.M., Marras M.A.,  
 CC "Generation and initial analysis of more than 15,000 full-length human  
 CC tyrosine kinase genes from the mouse cDNA sequences.";  
 CC and mouse cDNA sequences.";  
 CC proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DDJB databases.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 tyrosine phosphate.  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Prints; PR00401; SH2DOMAIN.  
 DR Prints; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00219; TyrKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR ATP-binding; Kinase; Nucleotide-binding; Transferase;  
 KW Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 368 AA; 42018 MW; 7AB6A53AFLA5059 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSVL  
 Q4FZR6 RAT PRELIMINARY; PRT; 379 AA.  
 AC Q4FZR6;  
 DT 30-AUG-2005, integrated into UniProtKB/TREMBL.  
 DT 30-AUG-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 7.  
 DE Lck\_mapped protein (Fragment).  
 GN Name=Lck\_mapped;  
 OS Rattus norvegicus (Rat).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 [1]

QY 1 TFDYLRSVL 9  
 Db 345 TFDYLRSVL 353

RESULT 2  
 Q4FZR6 RAT PRELIMINARY; PRT; 379 AA.  
 AC Q4FZR6;  
 DT 30-AUG-2005, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 7.  
 DE Lck\_mapped protein (Fragment).  
 GN Name=Lck\_mapped;  
 OS Rattus norvegicus (Rat).  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 [1]

QY 1 TFDYLRSVL 9  
 Db 356 TFDYLRSVL 364

RESULT 3  
 Q8QGJ9\_FUGRU PRELIMINARY; PRT; 502 AA.  
 ID Q8QGJ9;  
 DT 01-JUN-2002, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 16.  
 DE Lymphocyte-specific c-src family protein tyrosine kinase.  
 GN Name=LCK;  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;  
 OC Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC NCBITaxID=31033;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [mRNA].  
 RX MEDLINE=21874085; PubMed=11867707; DOI=10.1073/pnas.032680599;  
 RA Brenner S., Venkatesh B., Yap W.-H., Chou C.-F., Tay A.W.N.,  
 RA Ponniah S., Wang Y., Tan Y.H.;  
 RT "Conserved regulation of the lymphocyte-specific expression of lck in  
 the Fugu and mammals.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:2936-2941(2002).  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC EMBL; AF411956; AALB9664.1; -; Genomic\_DNA.  
 DR HSSP; P06239; IOPC.  
 DR Ensembl; SINFRUG0000129447; Fugu rubripes.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR00290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Kinase.  
 SQ SEQUENCE 502 AA; 57477 MW; A8C9EC2E774F79CD CRC64;

Query Match 100.0%; Score 45; DB 2; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSVL 9  
 Db 481 TFDYLRSVL 489

RESULT 4  
 LCK\_AOTNA STANDARD; PRT; 508 AA.  
 ID LCK\_AOTNA  
 AC Q5PKS1;

DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 08-NOV-2005, sequence version 3.  
 DT 07-MAR-2006, entry version 13.  
 DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)  
 DE (Lymphocyte cell-specific protein-tyrosine kinase).  
 GN Name=LCK;  
 OS Autus nancymae (Ma's night monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;  
 OC Autinae; Autus;  
 OC NCBITaxID=37293;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [mRNA].  
 RA Perez-Quintero L.A.; Vernet J.P.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Tyrosine kinase that plays an essential role for the  
 selection and maturation of developing T-cell in the thymus and in  
 mature T-cell function. Is constitutively associated with the  
 cytoplasmic portions of the CD4 and CD8 surface receptors and  
 plays a key role in T-cell antigen receptor(TCR)-linked signal  
 transduction pathways. Association of the TCR with a peptide  
 antigen-bound MHC complex facilitates the interaction of CD4 and  
 CD8 with MHC class II and class I molecules, respectively, and  
 thereby recruits the associated LCK to the vicinity of the TCR/CD3  
 complex. LCK then phosphorylates tyrosines residues within the  
 immunoreceptor tyrosines-based activation motifs (ITAMs) in the  
 cytoplasmic tails of the TCRgamma chains and CD3 subunits,  
 initiating the TCR/CD3 signaling pathway. In addition, contributes  
 to signaling by other receptor molecules. Associates directly with  
 the cytoplasmic tail of CD2, and upon engagement of the CD2  
 molecule, LCK undergoes hyperphosphorylation and activation. Also  
 plays a role in the IL2 receptor-linked signaling pathway that  
 controls T-cell proliferative response. Binding of IL2 to its  
 receptor results in increased activity of LCK. Is expressed at all  
 stages of thymocyte development and is required for the regulation  
 of maturation events that are governed by both pre-TCR and mature  
 alpha beta TCR (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein  
 tyrosine phosphate.  
 CC -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface  
 receptors, such as CD2, CD4, CD5, CD44, CD45 and CD122. Also  
 binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to  
 other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds  
 to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes  
 through its SH3 domain and to the tyrosine phosphorylated form of  
 KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.  
 CC Interacts with phosphorylated LME1. Interacts with CBLB (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.  
 CC Present in lipid rafts in an unactive form (By similarity).  
 CC -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.  
 CC Interaction is regulated by Ser-58 phosphorylation (By  
 similarity).  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 1 SH2 domain.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC EMBL; AY821852; AAV70114.2; -; mRNA.  
 DR SMR; Q5PKS1; 64-508.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR01452; SH3.  
 DR InterPro; IPR01245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.

RA	Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F., DR PRINTS; PR00452; SH3 DOMAIN.
RA	Wilson C.B.; DR PRINTS; PR00109; TYRKINASE.
RT	"Structure and expression of lck transcripts in human lymphoid cells.";
DR	ProDom; PD00001; Prot kinase; 1.
DR	ProDom; PD000066; SH3; 1.
DR	SMART; SM00252; SH2; 1.
DR	SMART; SM00326; SH3; 1.
DR	SMART; SM00219; TyrkC; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW	ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT	INIT_MET 0 0
FT	CHAIN 1 508
FT	ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase. Probable.
FT	Proto-oncogene tyrosine-protein kinase LCK; /FTId=PRO_0000088123.
FT	DOMAIN 60 120
FT	DOMAIN 126 223
FT	DOMAIN 244 497
FT	NP_BIND 250 258
FT	REGION 1 71
FT	ACT_SITE 363 363
FT	BINDING 272 272
FT	MOD_RES 393 393
FT	MOD_RES 504 504
FT	LIPID 1 1
FT	LIPID 2 2
FT	SEQUENCE 4 4
Qy	Query Match
Qy	Best Local Similarity 100.0%; Pred. No. 3.2;
Qy	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 TFDYLRSQL 9 485 TFDYLRSQL 493
RESULT 5	LCK_HUMAN
ID	LCK_HUMAN STANDARD; PRT; 508 AA.
AC	P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT	01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT	01-FEB-1994, sequence version 5.
DT	07-MAR-2006, entry version 87.
DE	Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (LCK) (T cell-specific protein-tyrosine kinase).
DE	Name=LCK;
GN	Homo sapiens (Human).
OS	Eukaryota; Chordata; Craniata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; OC Homo.
RN	NCBI_TaxID=9606;
RP	NUCLEOTIDE SEQUENCE [mRNA]; [1]
RX	MEDLINE=87133831; PubMed=3493153;
RA	Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y., Mak T.W.;
RT	"A human T cell-specific cDNA clone (YR16) encodes a protein with extensive homology to a family of protein-tyrosine kinases.";
RL	Eur. J. Immunol. 16:1643-1646(1986).
RN	[2]
RP	NUCLEOTIDE SEQUENCE [mRNA]; MEDLINE=89123626; PubMed=3265417;
RA	Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F., Wilson C.B.; DR PRINTS; PR00109; TYRKINASE.
RT	"Structure and expression of lck transcripts in human lymphoid cells.";
DR	ProDom; PD00001; Prot kinase; 1.
DR	ProDom; PD000066; SH3; 1.
DR	SMART; SM00252; SH2; 1.
DR	SMART; SM00326; SH3; 1.
DR	SMART; SM00219; TyrkC; 1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW	ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.
FT	INIT_MET 0 0
FT	CHAIN 1 508
FT	ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase. Probable.
FT	Proto-oncogene tyrosine-protein kinase LCK; /FTId=PRO_0000088123.
FT	DOMAIN 60 120
FT	DOMAIN 126 223
FT	DOMAIN 244 497
FT	NP_BIND 250 258
FT	REGION 1 71
FT	ACT_SITE 363 363
FT	BINDING 272 272
FT	MOD_RES 393 393
FT	MOD_RES 504 504
FT	LIPID 1 1
FT	LIPID 2 2
FT	SEQUENCE 4 4
Qy	Query Match
Qy	Best Local Similarity 100.0%; Pred. No. 3.2;
Qy	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 TFDYLRSQL 9 485 TFDYLRSQL 493
RESULT 5	LCK_HUMAN
ID	LCK_HUMAN STANDARD; PRT; 508 AA.
AC	P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT	01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT	01-FEB-1994, sequence version 5.
DT	07-MAR-2006, entry version 87.
DE	Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (LCK) (T cell-specific protein-tyrosine kinase).
DE	Name=LCK;
GN	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.
RN	NCBI_TaxID=9606;
RP	NUCLEOTIDE SEQUENCE [mRNA]; [1]
RX	MEDLINE=89096891; PubMed=2850479;
RA	Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;
RT	"Structure of the murine lck gene and its rearrangement in a murine lymphoma cell line";
RL	Mol. Cell. Biol. 8:3058-3064(1988).
RN	[9]
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.
RX	MEDLINE=89313764; PubMed=2787474;
RA	Takadera T., Leung S., Gernone A., Koga Y., Takihara Y., Miyamoto N.G., Mak T.W.;
RT	"Structure of the two promoters of the human lck gene: differential accumulation of two classes of lck transcripts in T cells.";
RL	Mol. Cell. Biol. 9:2173-2180(1989).
RN	[10]

RP NUCLEOTIDE SEQUENCE [mRNA] OF 13-508.  
 RC TISSUE=Peripheral blood lymphocyte;  
 RX MEDLINE=20462621; PubMed=11009097;  
 DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;  
 RA Boncristiano M., Majolini M.B., D'Ellos M.M., Pacini S., Valensin S.,  
 RA Ulivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,  
 RA Baldari C.T.;  
 RT "Defective recruitment and activation of ZAP-70 in common variable immunodeficiency patients with T cell defects.";  
 RL Eur. J. Immunol. 30:2632-2638 (2000).  
 RN [11]

RP NUCLEOTIDE SEQUENCE [mRNA] OF 367-508.  
 RX MEDLINE=88217332; PubMed=2835736;  
 RA Veillette A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.;  
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma and other non-lymphoid human tumor cell lines.";  
 RL Oncogene Res. 1:357-374 (1987).  
 RN [12]

RP NUCLEOTIDE SEQUENCE [mRNA] OF 374-508.  
 RX MEDLINE=8700726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;  
 RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,  
 RA Linna T.J.;  
 RT "Human T lymphocytes express a protein-tyrosine kinase homologous to p56LSTRA.";  
 RT Biochim. Biophys. Acta 888:286-295 (1986).  
 RN [13]

RP PHOSPHORYLATION SITE TYR-504.  
 RX MEDLINE=92347326; PubMed=1639064;  
 RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,  
 RA Amrein K.E., Autero M., Burn P., Ajitao K.;  
 RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and down regulates its catalytic activity.";  
 RL EMBO J. 11:2919-2924 (1992).  
 RN [14]

RP INTERACTION WITH PI3K.  
 RX MEDLINE=94067101; PubMed=7504174;  
 RA Vogel L.B., Fujita D.J.;  
 RT "The SH3 domain of p56lck is involved in binding to phosphatidylinositol 3'-kinase from T lymphocytes.";  
 RL Mol. Cell. Biol. 13:7408-7417 (1993).  
 RN [15]

RP INTERACTION WITH KHDRBS1.  
 RX MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;  
 RA Vogel L.B., Fujita D.J.;  
 RT "p70 phosphorylation and binding to p56lck is an early event in interleukin-2-induced onset of cell cycle progression in T-lymphocytes.";  
 RL J. Biol. Chem. 270:2506-2511 (1995).  
 RN [16]

RP INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.  
 RX PubMed=8618896;  
 RA Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;  
 RT "Phosphotyrosine-independent binding of a 62-kDa protein to the src homology 2 (SH2) domain of p56lck and its regulation by phosphorylation of Ser-59 in the lck unique N-terminal region.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342 (1995).  
 RN [17]

RP INTERACTION WITH HIV-1 NEF.  
 RX MEDLINE=96386556; PubMed=8794306;  
 RA Greenway A.L., Azad A., Mills J., McPhee D.A.;  
 RT "Human immunodeficiency virus type 1 Nef binds directly to LCK and mitogen-activated protein kinase, inhibiting kinase activity.";  
 RL J. Virol. 70:6701-6708 (1996).  
 RN [18]

RP REVIEW.  
 RX PubMed=10848956;  
 RA Isakov N., Biesinger B.;  
 RT "Lck protein tyrosine kinase is a key regulator of T-cell activation and a target for signal intervention by Herpesvirus saimiri and other viral gene products.";  
 RL Eur. J. Biochem. 267:3413-3421 (2000).  
 RN [19]

RP SUBCELLULAR LOCATION.

RX PubMed=12218089;  
 RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,  
 RA Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;  
 RT "Fyn is essential for tyrosine phosphorylation of Csk-binding protein/phosphoprotein associated with glycolipid-enriched microdomains in lipid rafts in resting T cells.";  
 RT J. Immunol. 169:2813-2817 (2002).  
 RL RN [20]

RP MASS SPECTROMETRY.  
 RX TISSUE=Mammary cancer;  
 RA MEDLINE=21829512; PubMed=11840567;  
 DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;  
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,  
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,  
 RA Zvelebil M.J.;  
 RT "Cluster analysis of an extensive human breast cancer cell line protein expression map database.";  
 RT Proteomics 2:212-223 (2002).  
 RL RN [21]

RP INTERACTION WITH LIME1.  
 RX PubMed=14610046; DOI=10.1084/jem.20031484;  
 RA Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,  
 RA Hilgert I., Paces J., Simeoni L., Klische S., Merten C., Schraven B.,  
 RA Horejsi V.;  
 RT "LIME: a new membrane raft-associated adaptor protein involved in CD4 and CD8 coreceptor signaling.";  
 RT J. Exp. Med. 198:1453-1462 (2003).  
 RL RN [22]

RP INTERACTION WITH LIME1.  
 Query Match 100.0%; Score 45; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 TFDYLRSLV 9
Db	485 TFDYLRSLV 493

RESULT 6

LCK_MOUSE	ID	LCK_MOUSE	STANDARD	PRT	508 AA.
AC	P06240; Q61794; Q61795; Q62320; Q91X65;				
DT	01-JAN-1988, integrated into UniProtKB/Swiss-Prot.				
DT	25-OCT-2005, sequence version 3.				
DT	07-MAR-2006, entry version 74.				
DE	Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)				
GN	Name=Lck; Synonyms=Lsk-t;				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
OC	NCBI_TAXID=10090;				
OX					
RN					

RP NUCLEOTIDE SEQUENCE [mRNA].  
 RX MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;  
 RA Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;  
 RT "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed in the murine T cell lymphoma LSTRA.";  
 RT Cell 43:393-404 (1985).  
 RL RN [2]

RP NUCLEOTIDE SEQUENCE [mRNA].  
 RX MEDLINE=86146842; PubMed=3081813;  
 RA Voronova A.F., Sefton B.M.;  
 RT "Expression of a new tyrosine protein kinase is stimulated by retrovirus promoter insertion.";  
 RL Nature 319:682-685 (1986).  
 RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].  
 STRAIN=NOD; TISSUE=Thymus;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., RT  
 RA Bjelic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., RT  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., RT  
 RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., RL  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., RN  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., RX  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., RA  
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., RT  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., RT  
 RA Georgi-Hemming P., Gingeras T.R., Gojobori T., Green R.E., RT  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., RN  
 RA Hill D., Hummieckl L., Iacono M., Ikeo K., Iwama A., Ishikawa T., [8]  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., RP  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., AND CYS-22.  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., RX  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., RA  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Littman D.R.;  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).  
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ringwald M., RT  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., RT  
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., RT  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., RT  
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K., RT  
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., RT  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., RT  
 RA Yamamoto H., Zaborsky E., Zhu S., Zimmer A., Hide W., Bult C., RT  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., RT  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., RN  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., [9]  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., RP  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., "Avian reovirus mRNAs are nonfunctional in infected mouse cells:  
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., "Interaction of the unique N-terminal region of tyrosine kinase p56lck  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., with cytoplasmic domains of CD4 and CD8 is mediated by cysteine  
 RA Hayashizaki Y., motifs."; Mol. Cell. Biol. 12:200-207 (2002).  
 RA "The transcriptional landscape of the mammalian genome."; Cell 60:755-765 (1990).  
 RN [10]

RA "Two lck transcripts containing different 5' untranslated regions are  
 RA present in T cells."; Mol. Cell. Biol. 7:4407-4413 (1987).  
 RA [7]

RA "Avian reovirus mRNAs are nonfunctional in infected mouse cells:  
 RA translational basis for virus host-range restriction.";  
 RA Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).

RA Amrein K.E., Sefton B.M.; [8]

RA INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS-CYS-4; CYS-19  
 RA AND CYS-22.  
 RA MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;  
 RA Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,  
 RA Littman D.R.;  
 RA "Interaction of the unique N-terminal region of tyrosine kinase p56lck  
 RA with cytoplasmic domains of CD4 and CD8 is mediated by cysteine  
 RA motifs.";  
 RA Cell 60:755-765 (1990).  
 RN [9]

RA MUTAGENESIS.  
 RA MEDLINE=93059594; PubMed=1279202;  
 RA Hurley T.R., Amrein K.E., Sefton B.M.;  
 RA "Creation and characterization of temperature-sensitive mutants of the  
 RA lck tyrosine protein kinase.";  
 RA J. Virol. 66:7406-7413(1992).  
 RN [10]

RA MUTAGENESIS OF LYS-272.  
 RA MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;  
 RA Abraham N., Miceli M.C., Parnes J.C., Veillette A.;  
 RA "Enhancement of T-cell responsiveness by the lymphocyte-specific  
 RA tyrosine protein kinase p56lck.";  
 RA Nature 350:62-66 (1991).  
 RL [11]

RA MUTAGENESIS OF TYR-504.  
 RA MEDLINE=91219495; PubMed=1708890;  
 RA Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;  
 RA "Thymic tumorigenesis induced by overexpression of p56lck.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).  
 RN [12]

RA PHOSPHORYLATION BY CSK.  
 RA PubMed=8371758; DOI=10.1038/365156a0;  
 RA Chow L.M., Fournel M., Davidson D., Veillette A.;  
 RA "Negative regulation of T-cell receptor signalling by tyrosine protein  
 RA kinase p50csk.";  
 RA Nature 365:156-160 (1993).  
 RN [13]

RA MUTAGENESIS.  
 RA MEDLINE=93133805; PubMed=8421674;  
 RA Carrera A.C., Alexandrov K., Roberts T.M.;  
 RA "The conserved lysine of the catalytic domain of protein kinases is  
 RA actively involved in the phosphotransfer reaction and not required for  
 RA anchoring ATP.";  
 RA Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).  
 RN [14]

RA PALMITOYLATION.  
 RA MEDLINE=94019312; PubMed=8413237;  
 RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;  
 RA "Palmitylation of an amino-terminal cysteine motif of protein tyrosine  
 RA kinases p56lck and p59fyn mediates interaction with glycosyl-  
 RA phosphatidylinositol-anchored proteins.";  
 RA Mol. Cell. Biol. 13:6385-6392(1993).  
 RN [15]

RA PALMITOYLATION.  
 RA MEDLINE=89096891; PubMed=2850479;  
 RA Garvin A.M., Pawar S., March J.D., Perlmutter R.M.;  
 RA "Structure of the murine lck gene and its rearrangement in a murine  
 RA lymphoma cell line.";  
 RA Mol. Cell. Biol. 8:3058-3064(1988).  
 RN [6]

RA NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.  
 RA MEDLINE=88142832; PubMed=3501824;  
 RA Voronova A.F., Adler H.T., Sefton B.M.;  
 RN [16]

RA INTERACTION WITH CBLB.  
 RA PubMed=10646608; DOI=10.1038/35003228;

RA Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T., RA Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A., RA Ittie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S., RA Penninger J.M.; "Negative regulation of lymphocyte activation and autoimmunity by the molecular adaptor Cbl-b."; RT Nature 403:211-216 (2000). RL [17]

RN SUBCELLULAR LOCATION.

RX PubMed=12218089;

RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T., RA Minaki Y., Kato A., Tani-Ichi S., Hamaka T., Kosugi A.; RT "Fyn is essential for tyrosine phosphorylation of Csk-binding protein/phosphoprotein associated with glycolipid-enriched microdomains in lipid rafts in resting T cells."; RL J. Immunol. 169:2813-2817 (2002).

RN [18]

RP PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.

RX PubMed=15592455; DOI=10.1038/nbt1046; Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H., RA Zha X.-M., Polakiewicz R.D., Comb M.J.; RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer

Query Match 100.0%; Score 45; DB 1; Length 508;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSQL 9

AC ||||| | | |

Db 485 TFDYLRSQL 493

RESULT 7

LCK\_SAISC ID LCK\_SAISC STANDARD; PRT; 508 AA.

AC Q95KR7;

DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.

DT 08-NOV-2005, sequence version 2.

DT 07-MAR-2006, entry version 26.

DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)

DE (Lymphocyte cell-specific protein-tyrosine kinase).

GN Name=LCK;

OS Saimiri sciureus (Common squirrel monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;

OC Cebinae; Saimiri.

NCBI\_TaxID=9521;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA], ENZYME REGULATION, AND INTERACTION WITH TISSUE HERPESVIRUS 2 TIP.

RC MEDLINE=21424508; PubMed=11533187;

RX DOI=10.1128/JVI.75.19.9252-9261.2001; Greve T., Tamgueney G., Fleischner B., Broeker B.M.; RA "Downregulation of p56Lck tyrosine kinase activity in T cells of squirrel monkeys (Saimiri sciureus) correlates with the non-transforming and apathogenic properties of herpesvirus saimiri in its natural host."; RL J. Virol. 75:9252-9261 (2001).

CC -!- FUNCTION: Tyrosine kinase that plays an essential role for the selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor (TCR)-linked signal transduction pathways. Association of the TCR with a peptide antigen-bound MHC complex facilitates the interaction of CD4 and CD8 with MHC class II and class I molecules, respectively, and thereby recruits the associated LCK to the vicinity of the TCR/CD3 complex. LCK then phosphorylates tyrosines residues within the immunoreceptor tyrosines-based activation motifs (ITAMs) in the cytoplasmic tails of the TCRgamma chains and CD3 subunits, initiating the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with

the cytoplasmic tail of CD2, and upon engagement of the CD2 molecule, LCK undergoes hyperphosphorylation and activation. Also plays a role in the IL2 receptor-linked signaling pathway that controls T-cell proliferative response. Binding of IL2 to its receptor results in increased activity of LCK. Is expressed at all stages of thymocyte development and is required for the regulation of maturation events that are governed by both pre-TCR and mature alpha beta TCR (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine phosphate.

CC -!- ENZYME REGULATION: Regulated by phosphatases.

CC -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1. Interacts with phosphorylated LIMEL. Interacts with CBLB (By similarity). Interacts with saimirine herpesvirus 2 TIP.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane. Present in lipid rafts in an unactive form (By similarity).

CC -!- TISSUE SPECIFICITY: Expressed specifically in lymphoid cells.

CC -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout T-cell ontogeny.

CC -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1. Interaction is regulated by Ser-58 phosphorylation (By similarity).

CC -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This phosphorylation downregulates catalytic activity. Phosphorylated on Tyr-393 either by itself or another kinase, leading to increased enzymatic activity.

CC -!- SIMILARITY: Belongs to the Tyr protein kinase family.

CC -!- STMLRITY: Contains 1 SH2 domain.

CC CAUTION: LCK seems to be active in all vertebrates, except in squirrel monkey T-cells, in which it is inactivated. The reason seems to be that squirrel monkey are the natural host for Saimiriine herpesvirus 2, which is able to efficiently transform T-cells through a mechanism involving viral Tip/ host LCK interaction. Its inactivation may a mechanism that specifically counteracts the transformation effects of viral Tip.

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CC DR EMBL: AJ277921; CAC38871.1; -; mRNA.

CC DR HSSP; P06239; 1LCK.

CC DR SMR; Q95KR7; 64-508.

CC DR InterPro; IPR000719; Prot kinase.

CC DR InterPro; IPR002290; Ser\_Thr\_Pkinase.

CC DR InterPro; IPR000980; SH2.

CC DR InterPro; IPR001452; SH3.

CC DR InterPro; IPR001245; Tyr\_Pkinase.

CC DR InterPro; IPR008266; Tyr\_Pkinase\_AS.

CC DR Pfam; PF0714; Pkinase\_Tyr; 1.

CC DR Pfam; PF00017; SH2; 1.

CC DR Pfam; PF00018; SH3\_1; 1.

CC DR PRINTS; PR00401; SH2DOMAIN.

CC DR PRINTS; PR00452; SH3DOMAIN.

CC DR PRINTS; PR00109; TYRKINASE.

CC DR ProDom; PD000001; Prot\_kinase; 1.

CC DR ProDom; PD000093; SH2; 1.

CC DR ProDom; PD000066; SH3; 1.

CC DR SMART; SM00252; SH2; 1.

CC DR SMART; SM00326; SH3; 1.

CC DR SMART; SM00219; TyrK; 1.

CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

CC DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

CC DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

CC DR PROSITE; PS50001; SH2; 1.

CC DR PROSITE; PS50002; SH3; 1.

KW ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;

KW Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;  
 KW SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.  
 FT INIT\_MET 0 0  
 FT CHAIN 1 508  
 FT DOMAIN 60 120  
 FT DOMAIN 126 223  
 FT DOMAIN 244 497  
 FT NP\_BIND 250 258  
 FT REGION 1 71  
 FT ACT\_SITE 363 363  
 FT BINDING 272 272  
 FT MOD\_RES 393 393  
 FT MOD\_RES 504 504  
 FT LIPID 1 1  
 FT LIPID 2 2  
 FT LIPID 4 4  
 SQ SEQUENCE 508 AA; 58122 MW; 5088C64061853819 CRC64;

Query Match 100.0%; Score 45; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 3.2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
 Db 485 TFDYLRSQL 493

RESULT 8

ID Q7RTZ3\_HUMAN PRELIMINARY; PRT; 509 AA.

AC Q7RTZ3;

DT 15-DEC-2003, integrated into UniProtKB/TREMBL.

DT 15-DEC-2003, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Protein tyrosine kinase.

GN Name=LCK;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1] NUCLEOTIDE\_SEQUENCE;

RX MEDLINE=22289034; PubMed=12401726;

RA Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,  
 Naquet P., Matsuda F., Imbert J., Vialettes B.;

RT "No association between lck gene polymorphisms and protein level in  
 type 1 diabetes.";

RT Diabetes 51:3326-3330(2002).

RL -!- MISCELLANEOUS: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ third party annotation (TPA) entry.

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CC EMBL; BN000073; CAD55807.1; -; Genomic\_DNA.

CC HSSP; P06239; 1BHF.

DR SMR; Q7RTZ3; 65-509.

DR Ensembl; ENSG00000182866; Homo sapiens.

DR GO; GO:0045121; C:lipid raft; ISS.

DR GO; GO:000242; C:pericentriolar material; ISS.

DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

DR GO; GO:0042169; F:SH2 domain binding; ISS.

DR GO; GO:0006919; P:caspase activation; ISS.

DR GO; GO:003097; P:hemopoiesis; ISS.

DR GO; GO:0006917; P:induction of apoptosis; ISS.

DR GO; GO:0007242; P:intracellular signaling cascade; ISS.

DR GO; GO:0050870; P:positive regulation of T cell activation; ISS.

DR GO; GO:0050862; P:positive regulation of T cell receptor sign. . . ; ISS.

DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

DR GO; GO:0007265; P:Ras protein signal transduction; ISS.

DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.

DR GO; GO:0000074; P:regulation of progression through cell cycle; ISS.

DR GO; GO:0042493; P:response to drug; ISS.

DR GO; GO:0030217; P:T cell differentiation; ISS.

DR GO; GO:0006882; P:zinc ion homeostasis; ISS.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_pk kinase.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR InterPro; IPR001245; Tyr\_pk kinase.

DR InterPro; IPR0008266; Tyr\_pk kinase\_AS.

DR Pfam; PF07714; Pkinase\_Tyr; 1.

DR Pfam; PF00017; SH2; 1.

DR PRINTS; PR00018; SH3; 1; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; TYRKINASE.

DR ProDom; PD000001; Prot\_kinase; 1.

DR ProDom; PD000093; SH2; 1.

DR ProDom; PD000066; SH3; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PS00019; TYRKc; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

DR Kinase; 509 AA; 58001 MW; 44BFF0D43FFB420D CRC64;

Query Match 100.0%; Score 45; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 3.2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
 Db 486 TFDYLRSQL 494

RESULT 9

ID Q95M32\_9PRIM PRELIMINARY; PRT; 509 AA.

AC Q95M32\_9PRIM

DT 01-DEC-2001, integrated into UniProtKB/TREMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 18.

DE Lck protein.

GN Name=Lck;

OS Hylobates sp. (gibbon).

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Hylobatidae; Hylobates.

OX NCBI\_TaxID=9581;

RN [1] NUCLEOTIDE\_SEQUENCE.

RX MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;

RA Picard C., Greenway A., Holloway G., Olive D., Collette Y.;

RT "Interaction with simian Hck tyrosine kinase reveals convergent evolution of the Nef protein from simian and human immunodeficiency viruses despite differential molecular surface usage.";

RT virology 295:320-327(2002).

[2] NUCLEOTIDE\_SEQUENCE.

RP Picard C.;

RL Thesis (2001), Department of Experimental Oncology laboratory, U.

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CC  
 DR EMBL; AJ320182; CAC44027.1; -; mRNA.  
 DR HSSP; P06239; 1LCK.  
 DR SMR; Q95M32; 65-509.  
 GO; GO:0045121; C:lipid raft; ISS.  
 DR GO; GO:000242; C:pericentrioral material; ISS.  
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.  
 DR GO; GO:0004213; F:SH2 domain binding; ISS.  
 DR GO; GO:0006919; P:caspase activation; ISS.  
 DR GO; GO:003097; P:hemopoiesis; ISS.  
 DR GO; GO:0006917; P:induction of apoptosis; ISS.  
 DR GO; GO:007242; P:intracellular signaling cascade; ISS.  
 DR GO; GO:0050870; P:positive regulation of T cell activation; ISS.  
 DR GO; GO:00050862; P:positive regulation of T cell receptor sign. . . ; ISS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.  
 DR GO; GO:0007265; P:Ras protein signal transduction; ISS.  
 DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.  
 DR GO; GO:0000074; P:regulation of progression through cell cycle; ISS.  
 DR GO; GO:0042493; P:response to drug; ISS.  
 GO; GO:0030217; P:T cell differentiation; ISS.  
 GO; GO:0006882; P:zinc ion homeostasis; ISS.  
 InterPro; IPR000719; Prot\_kinase.  
 InterPro; IPR002290; Ser\_thr\_pk kinase.  
 InterPro; IPR000980; SH3.  
 InterPro; IPR001452; SH3.  
 InterPro; IPR001245; Tyr\_pk kinase.  
 InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 Pfam; PF007714; Pkinase\_Tyr; 1.  
 Pfam; PF00017; SH2; 1.  
 Pfam; PF00018; SH3\_1; 1.  
 Prints; PRO0401; SH2DOMAIN.  
 Prints; PR00452; SH3DOMAIN.  
 Prints; PR00109; TYRKINASE.  
 Prod0; PD000001; Prot\_kinase; 1.  
 Prod0; PD000093; SH2; 1.  
 SMART; SM00252; SH2; 1.  
 SMART; SM00326; SH3; 1.  
 SMART; SM00219; TYRK; 1.  
 PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 PROSITE; PS50001; SH2; 1.  
 PROSITE; PS50002; SH3; 1.  
 Sequence 509 AA; 57947 MW; F1BFE5C237C8DB7E CRC64;

RESULT 10  
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 AC Q3ZCM0;  
 DT 27-SEP-2005, integrated into UniProtKB/TREMBL.  
 DT 27-SEP-2005, sequence version 1.  
 DT 07-MAR-2006, entry version 6.  
 DE Hypothetical protein MGC126900.  
 GN Name=MGC126900;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE\_SEQUENCE.  
 RC STRAIN=Crossbred x Angus; TISSUE=Ileum;

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RA Moore S.; Alexander L.; Brownstein M.; Guan L.; Lobo S.; Meng Y.;  
 RA Tanaguchi M.; Wang Z.; Yu J.; Prange C.; Schreiber K.; Shenmen C.;  
 RA Wagner L.; Bala M.; Barbazuk S.; Barber S.; BabaKaff R.; Beland J.;  
 RA Chun E.; Del Rio L.; Gibson S.; Hanson R.; Kirkpatrick R.; Liu J.;  
 RA Matsuo C.; Mayo M.; Santos R.R.; Stott J.; Tsai M.; Wong D.;  
 RA Siddiqui A.; Holt R.; Jones S.J.; Marra M.A.;  
 RL Submitted (AUG-2005) to the EMBL/GenBank/DDJB databases.  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC EMBL; BC102046; AAI02047.1; -; mRNA.  
 DR GO; GO:0045121; C:lipid raft; ISS.  
 DR GO; GO:000242; C:pericentrioral material; ISS.  
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.  
 DR GO; GO:0004713; F:protein tyrosine kinase activity; ISS.  
 DR GO; GO:0042169; F:SH2 domain binding; ISS.  
 DR GO; GO:0050862; P:positive regulation of T cell receptor sign. . . ; ISS.  
 DR GO; GO:0006919; P:caspase activation; ISS.  
 DR GO; GO:0030097; P:hemopoiesis; ISS.  
 DR GO; GO:0006917; P:induction of apoptosis; ISS.  
 DR GO; GO:007242; P:intracellular signaling cascade; ISS.  
 DR GO; GO:0050870; P:positive regulation of T cell activation; ISS.  
 DR GO; GO:0050862; P:positive regulation of T cell receptor sign. . . ; ISS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.  
 DR GO; GO:0007265; P:Ras protein signal transduction; ISS.  
 DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.  
 DR GO; GO:0000074; P:regulation of progression through cell cycle; ISS.  
 DR GO; GO:0042493; P:response to drug; ISS.  
 DR GO; GO:0030217; P:T cell differentiation; ISS.  
 DR GO; GO:0006882; P:zinc ion homeostasis; ISS.  
 InterPro; IPR000719; Prot\_kinase.  
 InterPro; IPR002290; Ser\_thr\_pk kinase.  
 InterPro; IPR000980; SH2.  
 InterPro; IPR001452; SH3.  
 InterPro; IPR001245; Tyr\_pk kinase.  
 InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 Pfam; PF007714; Pkinase\_Tyr; 1.  
 Pfam; PF00018; SH3\_1; 1.  
 Prints; PRO0401; SH2DOMAIN.  
 Prints; PR00452; SH3DOMAIN.  
 Prints; PR00109; TYRKINASE.  
 Prod0; PD000001; Prot\_kinase; 1.  
 Prod0; PD000093; SH2; 1.  
 Prod0; PD00066; SH3; 1.  
 SMART; SM00252; SH2; 1.  
 SMART; SM00326; SH3; 1.  
 SMART; SM00219; TYRK; 1.  
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 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 PROSITE; PS50001; SH2; 1.  
 PROSITE; PS50002; SH3; 1.  
 Hypothetical protein.  
 Sequence 509 AA; 58116 MW; CE0E80DCD6D0F2F8 CRC64;

RESULT 11  
 Q573B4\_HUMAN PRELIMINARY; PRT; 516 AA.  
 ID Q573B4\_HUMAN PRELIMINARY; PRT; 516 AA.  
 AC Q573B4;  
 DT 10-MAY-2005, integrated into UniProtKB/TREMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE Proto-oncogene tyrosine-protein kinase LCK.

GN Name=LCK;  
 OS Homo sapiens (Human);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo;  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 TISSUE=Blood;  
 RX PubMed=16107303; DOI=10.1016/j.gene.2005.06.018;  
 RA Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,  
 RA Naquet P., Imbert J.;  
 RT "A rare mRNA variant of the human lymphocyte-specific protein tyrosine kinase LCK gene with intron B retention and exon 7 skipping encodes a putative protein with altered SH3-dependent molecular interactions.";  
 RT Gene 359:18-25 (2005).  
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 CC  
 DR EMBL; AB025546; BAA84736.1; -; mRNA.  
 DR HSSP; P06239; IQPC.  
 DR Q9U8V6; 1-249.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-Tyrosine kinase activity; IEA.  
 DR GO; GO:007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 KW Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 249 AA; 28636 MW; D7F37EE197EA580C CRC64;  
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 Db 226 TFDYLKSQL 234  
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 DE  
 GN OS Aspergillus oryzae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 OX NCBI\_TaxID=5062;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=RIB 40;  
 RX PubMed=16372010; DOI=10.1038/nature04300;  
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,  
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,  
 RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,  
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,  
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,  
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,  
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,  
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,  
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
 RA Kuwara S., Ogasawara N., Kikuchi H.,  
 OC Myxinidae; Eptatretinae; Eptatretus.  
 OX NCBI\_TaxID=7764;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20020330; PubMed=10552041;  
 RA Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.,  
 RT "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:";  
 RL Nature 438:1157-1161 (2005).  
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 CC  
 RT isoform duplications around the divergence of cyclostomes and  
 RT gnathostomes.";  
 RT J. Mol. Evol. 49:601-608 (1999).  
 RL CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine phosphate.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
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 CC  
 DR EMBL; AB025546; BAA84736.1; -; mRNA.  
 DR HSSP; P06239; IQPC.  
 DR Q9U8V6; 1-249.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-Tyrosine kinase activity; IEA.  
 DR GO; GO:006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 KW Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 249 AA; 28636 MW; D7F37EE197EA580C CRC64;  
 Query Match 93.3%; Score 42; DB 2; Length 249;  
 Best Local Similarity 88.9%; Pred. No. 6.3;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TFDYLRSQL 9  
 Db 226 TFDYLKSQL 234  
 DE Predicted protein.  
 DE ORFNames=A0090005001207;  
 DE  
 GN OS Aspergillus oryzae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
 OX NCBI\_TaxID=5062;  
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 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=RIB 40;  
 RX PubMed=16372010; DOI=10.1038/nature04300;  
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,  
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,  
 RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,  
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,  
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,  
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,  
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,  
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,  
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
 RA Kuwara S., Ogasawara N., Kikuchi H.,  
 OC Myxinidae; Eptatretinae; Eptatretus.  
 OX NCBI\_TaxID=7764;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20020330; PubMed=10552041;  
 RA Suga H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.,  
 RT "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:";  
 RL Nature 438:1157-1161 (2005).  
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 CC

DR EMBL; AP007151; BAES6158.1; -; Genomic\_DNA.  
 DR SEQUENCE 318 AA; 36042 MW; E93277F08DD08AA1 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSV 8  
 Db 150 TFDYLRSV 157

RESULT 14

Q4RNX3\_TETNG PRELIMINARY; PRT; 466 AA.

ID Q4RNX3;  
 AC Q4RNX3; integrated into UniProtKB/TREMBL.  
 DT 19-JUL-2005, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Chromosome 10 SCAF15009, whole genome shotgun sequence. (Fragment).

GN ORFNames=GSTENG00031368001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetradontoidea; Tetraodontidae; Tetraodon.

OX NCBI\_TaxID=99883;

RN [1]

RP NUCLEOTIDE\_SEQUENCE.

RX PubMed=15496914; DOI=10.1038/nature03025;

RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Basilia C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,  
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quétier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).

RN [2]

RP NUCLEOTIDE\_SEQUENCE.

RG Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 preliminary data.

CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell  
 cycle. It is required in higher cells for entry into S-phase and  
 mitosis. Component of the kinase complex that phosphorylates the  
 C-terminus of RNA Polymerase II. Catalytic component of  
 MPF (By similarity).

CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
 mature oocytes (By similarity).

CC -!- SIMILARITY: Contains 1 SH3 domain.

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CC EMBL; AB003358; BAA20078.1; -; mRNA.

CC DR HSSP; P08631; 1AD5.

CC DR SMR; O13064; 43-48B.

CC DR GO; GO:0005524; F:ATP binding; IEA.

CC DR GO; GO:004713; F:protein-tyrosine kinase activity; IEA.

CC DR GO; GO:0007242; P:intracellular signaling cascade; IEA.

CC DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

CC DR InterPro; IPR000719; Prot\_kinase.

CC DR InterPro; IPR002290; Ser\_thr\_Pkinase.

CC DR InterPro; IPR000980; SH2.

CC DR InterPro; IPR01452; SH3.

CC DR InterPro; IPR01245; Tyr\_Pkinase.

CC DR InterPro; IPR008266; Tyr\_Pkinase\_AS.

CC DR Pfam; PF0774; Pkinase\_Tyr; 1.

CC DR Pfam; PF00017; SH2; 1.

CC DR Pfam; PF00018; SH3\_1; 1.

CC DR PRINTS; PR00401; SH2DOMAIN.

CC DR PRINTS; PR00452; SH3DOMAIN.

CC DR PRINTS; PR00109; TYRKINASE.

CC DR ProDom; PD000001; Prot\_kinase; 1.

CC DR ProDom; PD000093; SH2; 1.

CC DR ProDom; PD000066; SH3; 1.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR01452; SH3.

DR InterPro; IPR001245; Tyr\_Pkinase.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3\_1; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

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DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

DR ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase.

FT NON\_TER 466 466 AA; 53437 MW; E35D93F87395B799 CRC64;

QY 1 TFDYLRSVL 9  
 Db 446 TFEYLRSVL 454

Query Match 91.1%; Score 41; DB 2; Length 466;  
 Best Local Similarity 88.9%; Pred. No. 19;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyrK; 1.  
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 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Kinase.

SQ SEQUENCE 488 AA; 55795 MW; B7E70668B6EA92B2 CRC64;

Query Match Best Local Similarity 91.1%; Score 41; DB 2; Length 488;  
 Matches 8; Conservative Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYLRSVL 9  
 Db 465 TFDYLQSVL 473

RESULT 16

Q3U6Q5 MOUSE PRELIMINARY; PRT; 491 AA.

ID Q3U6Q5\_MOUSE AC Q3U6Q5; DT 11-OCT-2005, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, sequence version 1.  
 DE Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830119M13 product:Yamaguchi sarcoma viral (v-yes-1) oncogene homolog, full insert sequence.  
 GN Name=Lyn;  
 OS Mus musculus (Mouse).  
 OC Mammalia; Buteraria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone marrow; MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RX Carninci P., Hayashizaki Y.; RT "High-efficiency full-length cDNA cloning.", Methods Enzymol. 303:19-44(1999). [2]

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone marrow; PubMed=16141072; DOI=10.1126/science.1112014;

RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bjelic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgini-Hemming P., Gingera T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummiecke L., Iacono M., Ikeno K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollrias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavani W.J., Pavesi G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Stirling S., Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamamoto H., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niromiya N., Nishio T., Okada M., Piessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watanuki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.; "The transcriptional landscape of the mammalian genome."; Science 309:1559-1563 (2005).

[3]

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone marrow; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chohtia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson i.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Peretea G., Pesole G., Petrosky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa T., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; Nature 420:563-573 (2002).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone marrow; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RX Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okuda T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

	SQ	SEQUENCE	491 AA;	56285 MW;	2C82015D510B1F59 CRC64;
RA		Query Match	91.1%	Score 41;	DB 2;
RA		Best Local Similarity	88.9%	Pred. No.	20;
RT		Matches	8;	Conservative	1;
RL		Mismatches	0;	Indels	0;
RN		Gaps	0;		
RP					
RC	Q8CEI0_MOUSE	PRELIMINARY;	PRT;	491 AA.	
RX	Q8CEI0_MOUSE				
RA	Q8CEI0;				
RA	01-MAR-2003,	integrated into UniProtKB/TREMBL.			
DT	01-MAR-2003,	sequence version 1.			
DT	07-FEB-2006,	entry version 21.			
DE	10 day old male pancreas cDNA,	RIKEN full-length enriched library,			
DE	clone:1810073A02 product:Yamaguchi sarcoma viral (v-yes-1) oncogene				
DE	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,				
RA	Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,				
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,				
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,				
RT	"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";				
RL	Genome Res. 10:1757-1771 (2000).				
RN					
RP					
RC	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=C57BL/6J; TISSUE=Bone marrow;				
RA	Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,				
RA	Hori F., Iida J., Imamura K., Itoh M., Kanagawa S.,				
RA	Kawaji J., Kojima M., Konno H., Matsumoto H., Nakamura M., Ninomiya N.,				
RA	Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,				
RA	Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,				
RA	Muramatsu M., Hayashizaki Y.,				
RL	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.				
CC					
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>				
CC	Distributed under the Creative Commons Attribution-NoDerivs License				
CC					
DR					
DR	NUCLEOTIDE SEQUENCE.				
DR	STRAIN=C57BL/6J; TISSUE=Pancreas;				
DR	PubMed=16141072; DOI=10.1126/science.1112014;				
DR	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carninci P., Hayashizaki Y.,				
RA	"High-efficiency full-length cDNA cloning."				
RA	Methods Enzymol. 303:19-44 (1999).				
RA					
RA	[2]				
RA	NUCLEOTIDE SEQUENCE.				
RA	STRAIN=C57BL/6J; TISSUE=Pancreas;				
RA	PubMed=16141072; DOI=10.1126/science.1112014;				
RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,				
RA	Oyama R., Hayashizaki Y.,				
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RA	Methods Enzymol. 303:19-44 (1999).				
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RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
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RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
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RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
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RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
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RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
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RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
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RA	Methods Enzymol. 303:19-44 (1999).				
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RA	PubMed=16141072; DOI=10.1126/science.1112014;				
RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carninci P., Hayashizaki Y.,				
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RA	Methods Enzymol. 303:19-44 (1999).				
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RA	PubMed=16141072; DOI=10.1126/science.1112014;				
RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carninci P., Hayashizaki Y.,				
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RA	Methods Enzymol. 303:19-44 (1999).				
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RA	STRAIN=C57BL/6J; TISSUE=Pancreas;				
RA	PubMed=16141072; DOI=10.1126/science.1112014;				
RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carninci P., Hayashizaki Y.,				
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RA	Methods Enzymol. 303:19-44 (1999).				
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RA	STRAIN=C57BL/6J; TISSUE=Pancreas;				
RA	PubMed=16141072; DOI=10.1126/science.1112014;				
RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carninci P., Hayashizaki Y.,				
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RA	Methods Enzymol. 303:19-44 (1999).				
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RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
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RA	Methods Enzymol. 303:19-44 (1999).				
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RA	STRAIN=C57BL/6J; TISSUE=Pancreas;				
RA	PubMed=16141072; DOI=10.1126/science.1112014;				
RA	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;				
RA	Carninci P., Hayashizaki Y.,				
RA	"High-efficiency full-length cDNA cloning."				
RA	Methods Enzymol. 303:19-44 (1999).				
RA					
RA	NUCLEOTIDE SEQUENCE.				
RA					

RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.; "The transcriptional landscape of the mammalian genome.";  
 RT Science 309:1559-1563 (2005). [3]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RX PubMed=16141073; DOI=10.1126/science.1112009;

RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 (Genome Network Core Team) and the FANTOM Consortium;

RT "Antisense Transcription in the Mammalian Transcriptome.";  
 Science 309:1564-1566 (2005). [4]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka T., Kiyosawa H.,  
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 Schriml L.M., Kanapin A., Matsuda H., Battalov S., Beisel K.W.,  
 Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J.,  
 Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mikl H.,  
 Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 Ravi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,  
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 Hirozane-Kishikawa T., Komo H., Nakamura M., Sakazume N., Sato K.,  
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002). [5]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=21085660; PubMed=12127851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka T.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 Kadota K., Matsuda H.A., Ashburner M., Battalov S., Casavant T.,  
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,  
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kotsuki S.,  
 Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001). [6]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000). [7]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RC PubMed=16141073; DOI=10.1126/science.1112009;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwake S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000). [8]

RN NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Pancreas;

RC PubMed=16141073; DOI=10.1126/science.1112009;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagaawa T., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasada D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyka T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RA Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
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 CC EMBL; AK028112; BAC25753.1; -; mRNA.  
 DR HSSP; P08631; 1AD5.  
 DR SMR; Q8CE10; 46-491.  
 DR Ensembl; ENSMUSG0000042228; Mus musculus.  
 DR MGI; MGI:96892; Lyn.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IDA.  
 DR GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.  
 DR GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.  
 DR InterPro; IPR000719; prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR01452; SH3.  
 DR InterPro; IPR01245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
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 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
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 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
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 DR SMART; SM00219; TyrKc; 1.

Query Match 91.1%; Score 41; DB 2; Length 491;  
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 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DT	23-NOV-2004,	sequence version 1.	
DT	07-FEB-2006,	entry version 8.	
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RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=CB; TISSUE=Bursa;		
RA	Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,		
RA	Fiedler P., Kutter S., Blagodatski A., Kostovska D., Kotter M.,		
RA	Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;		
RT	"Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis.";		
RL	Genome Biol. 6:R6-R6 (2005).		
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CC	Distributed under the Creative Commons Attribution-NoDerivs License		
DR	EMBL; AJ719465; CAG31124.1; -; mRNA.		
DR	SMR; Q5ZMB9; 46-492.		
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DR	InterPro; IPR000719; Prot kinase.		
DR	InterPro; IPR002290; Ser-thr_pk kinase.		
DR	InterPro; IPR000980; SH2.		
DR	InterPro; IPR001452; SH3.		
DR	InterPro; IPR001245; Tyr_pk kinase.		
DR	InterPro; IPR008266; Tyr_pk kinase_AS.		
DR	Pfam; PF00714; Pkinase_Tyr; 1.		
DR	Pfam; PF00017; SH2; 1.		
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DR	ProDom; PD000093; SH2; 1.		
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KW	Hypothetical protein.		
SQ	SEQUENCE 492 AA; 56202 MW; 69D2F0534E33CC1E CRC64;		
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Best Local Similarity	88.9%; Pred. No. 20;		
Matches	8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
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RESULT	19		
INTERACTION WITH EPSTEIN-BARR VIRUS LMP2A.	[6]		
Miller C.L., Burkhardt A.L., Lee J.H., Stealey B., Iongnecker R.,			
Bolen J.B., Kieff E.;			
"Integral membrane protein 2 of Epstein-Barr virus regulates reactivation from latency through dominant negative effects on protein-tyrosine kinases.";			
RESULT	19		

RL Immunity 2:155-166 (1995).  
 RN [7] PHOSPHORYLATION SITE TYR-507, AND MASS SPECTROMETRY.  
 RP PubMed=15592455; DOI=10.1038/nbt1046;  
 RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,  
 RA Zha X.-M., Polakiewicz R.D., Comb M.J.;  
 RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer  
 cells.";  
 RL Nat. Biotechnol. 23:94-101(2005).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 CC tyrosine phosphate.  
 CC SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.  
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 CC IsoId=P07948-1; Sequence=Displayed;  
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 CC IsoId=P07948-2; Sequence=VSP 005002;  
 CC -!- TISSUE SPECIFICITY: Expressed in primary neuroblastoma tumors.  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC  
 CC -!- subfamily.  
 CC -!- SIMILARITY: Contains 1 SH2 domain.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
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 CC DR EMBL; M16038; AAA59540.1; -; mRNA.  
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 CC DR PDB; 1W1F; NMR; A=60-122.  
 CC DR PDB; 1WA7; NMR; A=60-122.  
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 CC DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
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 CC DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 CC DR InterPro; IPR000980; SH2.  
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 CC DR PRINTS; PR00452; SH3DOMAIN.  
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 DR PROSITE; PS50002; SH3; 1.  
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Query Match 91.1%; Score 41; DB 1; Length 511;  
 Best Local Similarity 88.9%; Pred. No. 21;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
 Db 488 TFDYLQSVL 496

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 DT 01-NOV-1997; sequence version 3.  
 DT 07-MAR-2006; entry version 64.  
 DE Tyrosine-protein kinase Lyn (EC 2.7.1.112).  
 DE Name=Lyn;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciuromorphati;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OC NCBI\_TAXID=10090;  
 RN [1]  
 RP NUCLEOTIDE\_SEQUENCE [mRNA];  
 RX MEDLINE=91260688; PubMed=1710766;  
 RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A., Lock P.,  
 RA Dunn A.R.;  
 RT "Alternatively spliced murine lyn mRNAs encode distinct proteins.";  
 RL Mol. Cell. Biol. 11:3399-3406(1991).  
 RN [2]  
 RP NUCLEOTIDE\_SEQUENCE [mRNA];  
 RX MEDLINE=91203857; PubMed=2017160;  
 RA Yi T., Bolen J.B., Ihle J.N.;  
 RT "Hematopoietic cells express two forms of lyn kinase differing by 21  
 amino acids in the amino terminus.";

RL Mol. Cell. Biol. 11:2391-2398 (1991).  
 RN [3] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM LYN A).  
 RC STRAIN=Czech II; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.M.,  
 RA Fahey J., Heilton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4] NUCLEOTIDE SEQUENCE [mRNA] OF 363-431.  
 RX MEDLINE=90152381; PubMed=2482828; DOI=10.1016/0378-1119(89)90465-4;  
 RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;  
 RT "The application of the polymerase chain reaction to cloning members  
 of the protein tyrosine kinase family";  
 RL Gene 85:67-74 (1989).  
 RN [5] INTERACTION WITH LIME1.  
 RP PubMed=16249387; DOI=10.1182/blood-2005-05-1859;  
 RX Ahn E., Lee H., Yun Y.;  
 RA "LIME acts as a transmembrane adapter mediating BCR-dependent B-cell  
 activation";  
 RL Blood 107:1521-1527 (2006).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
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 CC -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=LYN A;  
 CC IsoId=P25911-1; Sequence=Displayed;  
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and  
 CC myeloid cells.  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC  
 CC -!- subfamily.  
 CC -!- SIMILARITY: Contains 1 SH2 domain.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
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 DR EMBL: BC031547; AAH31547.1; -; mRNA.  
 DR EMBL: M33426; AAA40017.1; -; mRNA.  
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 DR SMR; P25911; 66-51.  
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 DR MGI; MGI:96892; Lyn.  
 GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.  
 DR GO; GO:0046777; P:autophosphorylation; IDA.  
 GO; GO:0007242; P:intracellular signaling cascade; IDA.

DR GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.  
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 DR InterPro; IPR01452; SH3.  
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 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
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 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
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 KW Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;  
 KW SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.  
 FT INIT\_MET 0 0 By similarity.  
 FT CHAIN 1 511 Tyrosine-protein kinase LYN.  
 FT /FTId=PRO\_0000088130.  
 FT DOMAIN 62 122 SH3.  
 FT DOMAIN 128 225 SH2.  
 FT DOMAIN 246 500 Protein kinase.  
 FT NP\_BIND 252 260 ATP (By similarity).  
 FT ACT\_SITE 366 366 Proton acceptor (By similarity).  
 FT BINDING 274 274 ATP (By similarity).  
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 FT LIPID 2 2 S-palmitoyl cysteine (By similarity).  
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 DT 07-MAR-2006, entry version 57.  
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OC Muroidea; Muridae; Murinae; Rattus.  
 OC NCBI\_TAXID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [mRNA].  
 RA Minoguchi K., Nishikata H., Siraganian R.P.;  
 RT "Bacterially expressed rat p56lyn binds several proteins in rat  
 basophilic leukemia cells including pp72, a tyrosine phosphorylated  
 protein prominent in activated cells.";  
 RL J. Immunol. 150:222-222(1993).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [mRNA].  
 RX MEDLINE=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;  
 RA Rider L.G., Raben N., Miller L., Jelisema C.;  
 RT "The cDNAs encoding two forms of the LYN protein-tyrosine kinase are  
 expressed in rat mast cells and human myeloid cells.";  
 RL Gene 138:219-222 (1994).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [mRNA].  
 RX MEDLINE=97442484; PubMed=9295361; DOI=10.1074/jbc.272.38.24072;  
 RA Vonakics B.M., Chen H., Haleem-Smith H., Metzger H.;  
 RT "The unique domain as the site on Lyn kinase for its constitutive  
 association with the high affinity receptor for IgE.";  
 RL J. Biol. Chem. 272:24072-24080(1997).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 tyrosine phosphate.  
 CC -!- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.  
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 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC  
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 CC -!- SIMILARITY: Contains 1 SH3 domain.  
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 KW Alternative splicing; ATP-binding; Kinase; Lipoprotein; Myristate;  
 KW Nucleotide-binding; Palmitate; Phosphorylation; Proto-Oncogene;  
 KW SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.  
 FT INIT\_MET 0 0 By similarity.  
 FT CHAIN\_1 511 Tyrosine-protein kinase Lyn.  
 FT /FTId=PRO\_0000088131.  
 FT DOMAIN 62 122 SH3.  
 FT DOMAIN 128 225 SH2.  
 FT DOMAIN 246 500 Protein kinase.  
 FT NP\_BIND 252 260 ATP (By similarity).  
 FT ACT SITE 366 366 Proton acceptor (By similarity).  
 FT BINDING 274 274 ATP (By similarity).  
 FT MOD\_RES 396 396 Phosphotyrosine (by autocatalysis) (By similarity).  
 FT LIPID 1 1 N-myristoyl glycine (By similarity).  
 FT LIPID 2 2 S-palmitoyl cysteine (By similarity).  
 FT VARSPLIC 24 44 Missing (in isoform LYN B).  
 FT /FTId=VSP\_005004.  
 FT CONFLICT 230 230 P -> L (in Ref. 2).  
 FT CONFLICT 307 307 V -> A (in Ref. 2).  
 FT CONFLICT 418 418 C -> Y (in Ref. 2).  
 SQ SEQUENCE 511 AA; 58529 MW; 24A2E5E229CD43ED CRC64;

Query Match 91.1%; Score 41; DB 1; Length 511;  
 Best Local Similarity 88.9%; Pred. No. 21; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1 TFDYIYRSVL 9
Db	488 TFDYIYQSVL 496

RESULT 22  
 Q3TCS3\_MOUSE  
 ID Q3TCS3\_MOUSE PRELIMINARY; PRT; 512 AA.  
 AC Q3TCS3;  
 DT 11-OCT-2005, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 5.  
 DE NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched  
 library, clone:F630107015 product:Yamaguchi sarcoma viral (v-yes-1)  
 oncogene homolog, full insert sequence (Bone marrow macrophage cDNA,  
 DE RIKEN full-length enriched library, clone:I830054M12 product:Yamaguchi  
 DE sarcoma viral (v-yes-1) oncogene homolog, full insert sequence).  
 OS Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OC NCBI\_TAXID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Methods Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;  
 RA PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wellis C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batyalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Ambesi-Impiombato A., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Della Gatta G.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,



DR GO; GO:0004713; P:protein-tyrosine kinase activity; IDA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IDA.  
 DR GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.  
 DR GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR00980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Prints; PRO0452; SH2DOMAIN.  
 DR Prints; PR00109; TYRKINASE.  
 DR ProdDom; PD000001; Prot\_kinase; 1.  
 DR ProdDom; PD000093; SH2; 1.  
 DR ProdDom; PD000066; SH3; 1.

Query Match 91.1%; Score 41; DB 2; Length 512;  
 Best Local Similarity 88.9%; Pred. No. 21;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
 Db 489 TFDYIQLSQL 497

RESULT 23

Q6NUK7 HUMAN PRELIMINARY; PRT; 582 AA.  
 ID Q6NUK7\_HUMAN PRELIMINARY; PRT; 582 AA.  
 AC Q6NUK7;  
 DT 05-JUL-2004, integrated into UniProtKB/TREMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 19.  
 DE LYN protein (Fragment).  
 DE Name=LYN;  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC Homo sapiens (Human).  
 RN NCBI\_TAXID=9606;  
 RN {1}

RC NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Roquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RG NIH MGC Project;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

RN [3]

RN RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Placenta;  
 RC NIH MGC Project;  
 RG RL Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: May serve as part of a signaling pathway coupling the FC receptor to the activation of the respiratory burst. May also contribute to neutrophil migration and may regulate the degranulation process of neutrophils (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.

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CC EMBL; BC068551; AAH68551; 1; mRNA.  
 CC EMBL; BC059394; AAH59394; 1; mRNA.  
 CC HSSP; P08631; IAD5.

DR SMR; Q6NUK7; 24-86, 137-582.  
 DR Ensembl; ENSG0000147507; Homo sapiens.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0000165; F:nucleotide binding; IEA.  
 DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000108; Neu\_cyt\_fact\_2.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; Tyr\_pk kinase.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Prints; PR00499; P67PHOX.  
 DR Prints; PR00401; SH2DOMAIN.  
 DR Prints; PRO0452; SH3DOMAIN.  
 DR Prints; PR00109; TYRKINASE.  
 DR ProdDom; PD000001; Prot\_kinase; 1.  
 DR ProdDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 DR ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase;  
 KW Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 582 AA; 65809 MW; 1CFF99768C28E9BB CRC64;

Query Match 91.1%; Score 41; DB 2; Length 582;  
 Best Local Similarity 88.9%; Pred. No. 24;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TFDYLRSQL 9  
 Db 559 TFDYIQLSQL 567

RESULT 24

Q66104 BRARE PRELIMINARY; PRT; 510 AA.  
 ID Q66104\_BRARE PRELIMINARY; PRT; 510 AA.  
 AC Q66104;  
 DT 11-OCT-2004, integrated into UniProtKB/TREMBL.  
 DT , 11-OCT-2004, sequence version 1.  
 DT , 07-FEB-2006, entry version 11.

RL

DE Zgc:92124.  
 GN ORFNames=zgc:92124;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Whole;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole;  
 RA Director MGC Project;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
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 EMBL; BC081601; AAH81601.1; -; mRNA.  
 DR SMR; Q66104; 65-510  
 ENSMBL; ENSDARG0000031715; Danio rerio.  
 DR ZFIN; ZDB-GENE-040912-7; zgc:92124.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_Pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 SQ SEQUENCE 605 AA; 67156 MW; 086740E5B9FFC1AE CRC64;  
 Query Match 1 TFDYLRSV 8  
 Best Local Similarity 87.5%; Pred. No. 1e+02; Length 605;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy |||||:  
 Db 487 TFDYIQLSV 495  
 RN NUCLEOTIDE SEQUENCE.  
 RP RESULT 25  
 RC STRAIN=AF293 / CBS 101355 / FGSC A1100;  
 RX PubMed=16372009; DOI=10.1038/nature04332;  
 RA Nieman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,  
 RA Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,  
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,  
 RA Farman M., Fedorova N.D., Feldblyum T.V., Fischer R.,  
 RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,  
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,  
 RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,  
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,  
 RA Kulkarni R., Kumagai T., Lafont A., Latge J.-P., Li W., Lord A.,  
 RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,  
 RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neill S., Paulsen I.,  
 RA RabbinoWitsch E., Rawlins N., Rajandream M.A., Reichardt U.,  
 RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,  
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,  
 RA Machida M., Hall N., Barrell B.G., Denning D.W.;  
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
 Aspergillus fumigatus";  
 Nature 438:1151-1156 (2005).  
 !- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
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 CC EMBL; AAHF01000001; EAL93604.1; -; Genomic\_DNA.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 605 AA; 67156 MW; 086740E5B9FFC1AE CRC64;  
 Query Match 1 TFDYLRSV 8  
 Best Local Similarity 87.5%; Pred. No. 1e+02; Length 605;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy |||||:  
 Db 558 TFDYLRSV 565  
 RESULT 26  
 ID Q5AZN3\_EMENTI  
 AC Q5AZN3\_EMENTI PRELIMINARY; PRT; 606 AA.  
 DT 26-APR-2005, integrated into UniProtKB/TREMBL.

DT 26-APR-2005, sequence version 1.  
 DT 07-MAR-2006, entry version 6.  
 DE Hypothetical protein.  
 GN ORFNames=AN6247.2;  
 OS Aspergillus nidulans FGSC A4.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=227321;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=FGSC 4;  
 RX PubMed=16372000; DOI=10.1038/nature04341;  
 RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,  
 RA Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,  
 RA Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,  
 RA Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C.,  
 RA Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,  
 RA Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,  
 RA Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,  
 RA Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,  
 RA Caddick M., Hynes M., Paolletti M., Fischer R., Miller B.L., Dyer P.S.,  
 RA Sachs M.S., Osmani S.A., Birren B.W.;  
 RT "Sequencing of Aspergillus nidulans and comparative analysis with A.  
 RT fumigatus and A. oryzae.";  
 RL Nature 438:1105-1115 (2005).  
 CC !- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC-----  
 DR EMBL; AACD01000107; EAAS8631.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 606 AA; 67119 MW; A95532E982BF7A8E CRC64;

Query Match 84.4%; Score 38; DB 2; Length 606;  
 Best Local Similarity 87.5%; Pred. No. 1e+02;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TFDYILRSV 8  
 Db 560 TFDYILRSV 567

RESULT 27  
 Q86TW9 HUMAN PRELIMINARY; PRT; 98 AA.  
 AC Q86TW9;  
 DT 01-JUN-2003, integrated into UniProtKB/TREMBL.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE Full-length cDNA clone CS0DI065YF14 of Placenta of Homo sapiens  
 DE (human) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1] NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Placenta;  
 RA Li W.B., Gruber C., Jesse J., Polayes D.;  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBBJ databases.  
 RN [2] NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Placenta;  
 RA Genoscope;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBBJ databases.  
 RN [3] NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Placenta;  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBBJ databases.  
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 CC-----  
 DR EMBL; BX248053; CAD62355.1; -; mRNA.  
 DR Ensembl; ENSG00000119688; Homo sapiens.  
 FT NON\_TER 98 98  
 SQ SEQUENCE 98 AA; 10702 MW; B5072D6ETDADBFBB CRC64;  
 Query Match 82.2%; Score 37; DB 2; Length 98;  
 Best Local Similarity 77.8%; Pred. No. 25;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TFDYILRSVL 9  
 Db 13 TFDYLGSL 21

RESULT 28  
 Q5FWT4 RAT ID Q5FWT4\_RAT PRELIMINARY; PRT; 267 AA.  
 AC Q5FWT4;  
 DT 01-MAR-2005, integrated into UniProtKB/TREMBL.  
 DT 01-MAR-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 8.  
 DE ATP-binding cassette, sub-family D (ALD), member 4 (Predicted).  
 Name=Abcd4;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;

[1]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Ovary;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sheenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL RN [2] NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Ovary;  
 RC NIH MGC Project;  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBBJ databases.  
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 CC-----  
 DR EMBL; BC089214; AAH89214.1; -; mRNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 KW ATP-binding.  
 SQ SEQUENCE 267 AA; 29257 MW; FA84B1C7FBB5B3D5 CRC64;

Query Match 82.2%; Score 37; DB 2; Length 267;  
 Best Local Similarity 77.8%; Pred. No. 71;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TFDYILRSVL 9  
 Db 50 TFDYLGSL 58

RESULT 29

Q8YMU7\_ANASP PRELIMINARY; PRT; 379 AA.

ID Q8YMU7\_ANASP PRELIMINARY; PRT; 379 AA.

AC Q8YMU7;

DT 01-MAR-2002, integrated into UniProtKB/TREMBL.

DT 01-MAR-2002, sequence version 1.

DT 07-FEB-2006, entry version 13.

DE Mannosyl transferase.

GN OrderedLocusNames=al14830;

OS Anabaena sp. (strain PCC 7120).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI\_TaxID=103690;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=21595285; PubMed=11759840; DOI=10.1093/dnarecs/8.5.205;

RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

RA Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;

RT "Complete genomic sequence of the filamentous nitrogen-fixing

cyanobacterium Anabaena sp. strain PCC 7120.";

RT DNA Res. 8:205-213 (2001).

RL

CC

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CC

DR EMBL; BA000019; BAB76529.1; -; Genomic\_DNA.

DR PIR; AF2409; AF2409.

DR BioCyc; NSP103690:ALL4830-MONOMER; -.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0009058; P:biosynthesis; IEA.

DR InterPro; IPR001296; Glyco\_transf\_1.

DR Pfam; PF00534; Glycos\_transf\_1; 1.

DR Complete proteome; Transferase.

SQ SEQUENCE 381 AA; 43616 MW; 881A8010B2BB24B6 CRC64;

Query Match 82.2%; Score 37; DB 2; Length 381;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 TFDYLRs 132

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Search completed: June 29, 2006, 09:29:35

Job time : 109.942 secs

RESULT 30

Q3MBB4\_ANAVT PRELIMINARY; PRT; 381 AA.

Q3MBB4\_ANAVT PRELIMINARY; PRT; 381 AA.

ID Q3MBB4\_ANAVT PRELIMINARY; PRT; 381 AA.

AC Q3MBB4;

DT 25-OCT-2005, integrated into UniProtKB/TREMBL.

DT 25-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE Glycosyl transferase, group 1.

GN ORFNames=Ava\_2100;

OS Anaabaena variabilis (strain ATCC 29413).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.

OX NCBI\_TaxID=240292;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 29413;

RG US DOE Joint Genome Institute;

RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israeni S., Pitluck S., Saunders E.H., Schmutz J., Lariner F., Land M., Kyrpides N., Mavromatis K., Richardson P.; RT "Complete sequence of Anabaena variabilis ATCC 29413.";

RL Submitted (SEP-2005) to the EMBL/GenBank/DDJB databases.

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CC

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 117.59 seconds  
(without alignments)  
78.664 Million cell updates/sec

Title: US-10-062-257A-2  
Perfect score: 51  
Sequence: 1 DYLRSVLEDF 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_7.2;\*  
1: uniprot\_sprot:/\*  
2: uniprot\_trembl:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	51	100.0	502 2 Q8QGJ9_FUGRU	Q8qgj9 fugu rubrif
2	51	100.0	508 1 LCK_AOTNA	Q5pxs1 aotus nancyc
3	51	100.0	508 1 LCK_HUMAN	P06239 homo sapien
4	51	100.0	508 1 LCK_SAISC	Q95kr7 saimiri sci
5	51	100.0	509 2 Q7RTZ3_HUMAN	Q7rtz3 homo sapien
6	51	100.0	509 2 Q95M32_9PRIM	Q95m32 hylobates s
7	51	100.0	509 2 Q3ZCM0_BOVIN	Q3zcm0 bos taurus
8	51	100.0	516 2 Q573B4_HUMAN	Q573b4 homo sapiem
9	48	94.1	249 2 Q9U8V6_EPTBU	Q9u8v6 eptatretus
10	48	94.1	368 2 Q3TLX4_MOUSE	Q3tlx4 mus musculus
11	48	94.1	379 2 Q4FZR6_RAT	Q4fzr6 rattus norve
12	48	94.1	508 1 LCK_MOUSE	P06240 mus musculus
13	47	92.2	466 2 Q4RNX3_TETNG	Q4rnx3 tetraodon m
14	44	86.3	488 2 O13064_XENLA	O13064 xenopus lae
15	44	86.3	491 2 Q3U6Q5_MOUSE	Q3u6q5 mus musculus
16	44	86.3	491 2 Q8CEI0_MOUSE	Q8cei0 mus musculus
17	44	86.3	492 2 Q5ZMB9_CHICK	Q5zmb9 gallus gallu
18	44	86.3	511 1 LYN_HUMAN	P07948 homo sapien
19	44	86.3	511 1 LYN_MOUSE	P25911 mus musculus
20	44	86.3	511 1 LYN_RAT	Q07014 rattus norve
21	44	86.3	512 2 Q3TCS3_MOUSE	Q3tcs3 m nod-deriv
22	44	86.3	582 2 Q6NUK7_HUMAN	Q6nuk7 homo sapien
23	43	84.3	502 2 Q9DDK6_SALSA	Q9ddk6 salmo salar
24	43	84.3	503 2 Q6TPQ4_BRARE	Q6tpq4 brachydanio
25	42	82.4	496 2 Q93411_XENLA	Q93411 xenopus lae
26	42	82.4	507 1 LCK_CHICK	P42683 gallus gallu
27	42	82.4	510 2 Q66I04_BRARE	Q66i04 brachydanio
28	40	78.4	196 2 Q5RHX5_BRARE	Q5rhx5 brachydanio
29	40	78.4	280 1 DCNL4_BRARE	Q5rnx6 brachydanio
30	40	78.4	281 2 Q4RKU7_TETNG	Q4rku7 tetraodon n
31	40	78.4	396 2 Q3A1V4_PELLCD	Q3a1v4 pelobacter

32	78.4	509	STK_HYDAT
33	39	39	Q9VWB1_DROME
34	76.5	498	BLK_MOUSE
35	39	76.5	Q5FW27_XENTR
36	39	76.5	Q3TAT8_MOUSE
37	39	76.5	Q4KM97_RAT
38	39	76.5	Q8K2M8_MOUSE
39	39	76.5	BLK_HUMAN
40	39	76.5	Q96TIN1_HUMAN
41	39	76.5	Q5UQF6_MIMIV
42	39	76.5	Q4CELO_CLOTM
43	39	76.5	Q9RLI6_PSEAE
44	38	74.5	Q8TZE4_PYRFU
45	38	74.5	184
46	38	74.5	260
47	38	74.5	340
48	38	74.5	364
49	38	74.5	377
50	38	74.5	403
51	38	74.5	455
52	38	74.5	503
53	38	74.5	502
54	38	74.5	1
55	38	74.5	2
56	38	74.5	2
57	38	74.5	523
58	38	74.5	1
59	38	74.5	525
60	38	74.5	2
61	38	74.5	2
62	38	74.5	528
63	38	74.5	570
64	38	74.5	580
65	38	74.5	529
66	38	74.5	580
67	38	74.5	580
68	38	74.5	1015
69	38	74.5	2343
70	38	74.5	1627
71	37	72.5	63
72	37	72.5	100
73	37	72.5	262
74	37	72.5	292
75	37	72.5	303
76	37	72.5	303
77	37	72.5	306
78	37	72.5	330
79	37	72.5	356
80	37	72.5	356
81	37	72.5	361
82	37	72.5	367
83	37	72.5	382
84	37	72.5	384
85	37	72.5	453
86	37	72.5	696
87	37	72.5	710
88	37	72.5	959
89	37	72.5	1444
90	37	72.5	2268
91	36	70.6	106
92	36	70.6	127
93	36	70.6	158
94	36	70.6	163
95	36	70.6	187
96	36	70.6	187
97	36	70.6	202
98	36	70.6	238
99	36	70.6	249
100	36	70.6	255

RESNIT 1  
 Q8QGJ9\_FUGRU PRELIMINARY; PRT; 502 AA.  
 AC DT  
 ID DT  
 DT 08-NOV-2005, integrated into UniProtKB/TREMBL.  
 DT 01-JUN-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 13.  
 DE Lymphocyte-specific c-src family protein tyrosine kinase.  
 GN Name=Lck;  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetradontoidea; Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21874085; PubMed=11867707; DOI=10.1073/pnas.032680599;  
 RA Brenner S., Venkatesh B., Yap W.-H., Chou C.-F., Tay A.W.N.,  
 RT "Conserved regulation of the lymphocyte-specific expression of lck in  
 the Fugu and mammals.", Proc. Natl. Acad. Sci. U.S.A. 99:2936-2941 (2002).  
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 CC EMBL; AF411956; AAL89664.1; - ; Genomic\_DNA.  
 DR HSSP; P06239; IOPC.  
 DR Ensembl; SINFRUG0000129447; Fugu rubripes.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR00290; Ser\_Thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM000252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Kinase.  
 SQ SEQUENCE 502 AA; 57477 MW; A8C9EC2E774F79CD CRC64;

Query Match 100.0%; Score 51; DB 2; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDF 10  
 Qy |||||||  
 Db 483 DYLRSVLED 492

RESULT 2  
 LCK\_AOTNA STANDARD; PRT; 508 AA.  
 AC DT  
 ID DT  
 DT 08-NOV-2005, sequence version 3.  
 DE 07-MAR-2006, entry version 13.  
 DE Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (p56-LCK)  
 DE (Lymphocyte cell-specific protein-tyrosine kinase).  
 GN Name=LCK;  
 OS Aotus nancymae (Ma's night monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;  
 OC Aotinae; Aotus.  
 OX NCBI\_TaxID=37293;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [mRNA].  
 RA Perez-Quintero L.A.; Vernot J.P.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: Tyrosine kinase that plays an essential role for the  
 selection and maturation of developing T-cell in the thymus and in  
 mature T-cell function. Is constitutively associated with the  
 cytoplasmic portions of the CD4 and CD8 surface receptors and  
 plays a key role in T-cell antigen receptor (TCR)-linked signal  
 transduction pathways. Association of the TCR with a peptide  
 antigen-bound MHC complex facilitates the interaction of CD4 and  
 CD8 with MHC class II and class I molecules, respectively, and  
 thereby recruits the associated LCK to the vicinity of the TCR/CD3  
 complex. LCK then phosphorylates tyrosines residues within the  
 immunoreceptor tyrosines-based activation motifs (ITAMs) in the  
 cytoplasmic tails of the TCRgamma chains and CD3 subunits,  
 initiating the TCR/CD3 signaling pathway. In addition, contributes  
 to signaling by other receptor molecules. Associates directly with  
 the cytoplasmic tail of CD2, and upon engagement of the CD2  
 molecule, LCK undergoes hyperphosphorylation and activation. Also  
 plays a role in the IL2 receptor-linked signaling pathway that  
 controls T-cell proliferative response. Binding of IL2 to its  
 receptor results in increased activity of LCK. Is expressed at all  
 stages of thymocyte development and is required for the regulation  
 of maturation events that are governed by both pre-TCR and mature  
 alpha beta TCR (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 tyrosine phosphate.  
 CC -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface  
 receptors, such as CD2, CD4, CD5, CD44, CD45 and CD122. Also  
 binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to  
 other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds  
 to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes  
 through its SH3 domain and to the tyrosine phosphorylated form of  
 KHDRBS1/p70 through its SH2 domain. Interacts with SOSTM1.  
 DR Interacts with CBLB (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane.  
 CC -!- DOMAIN: The SH2 domain mediates interaction with SOSTM1.  
 DR Interaction is regulated by Ser-58 phosphorylation (By  
 similarity).  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC  
 CC -!- SIMILARITY: Contains 1 SH2 domain.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
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 CC EMBL; AY821852; AAV70114.2; - ; mRNA.  
 DR SMR; Q5PXS1; 64-508.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR01452; SH3.  
 DR InterPro; IPR01245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.

DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS55001; SH2; 1.  
 DR PROSITE; PS55002; SH3; 1.  
 KW ATP-binding; Kinase; Lipoprotein; Membrane; Myristate;  
 KW Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene;  
 KW SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.  
 FT INIT\_MET 0 0  
 FT CHAIN 1 508  
 FT LCK /FTId=PRO\_0000088123.  
 FT DOMAIN 60 120  
 FT DOMAIN 126 223  
 FT DOMAIN 244 497  
 FT NP\_BIND 250 258  
 FT REGION 1 71  
 FT ACT\_SITE 363 363  
 FT BINDING 272 272  
 FT MOD\_RES 393 393  
 FT MOD\_RES 504 504  
 FT LIPID 1 1  
 FT LIPID 2 2  
 FT LIPID 4 4  
 SQ SEQUENCE 508 AA; 58041 MW; 8B61951BC192A3A4 CRC64;

RESULT 3

Query Match 100.0%; Score 51; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DYLRSVLEDF 10  
 Db 487 DYLRSVLEDF 496

RX MEDLINE=89123626; PubMed=3265417;  
 RA Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,  
 RA Wilson C.B.;  
 RT "Structure and expression of lck transcripts in human lymphoid  
 cells.";  
 RT J. Cell. Biochem. 38:117-126(1988).  
 RL RN [3]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;  
 RA Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,  
 RA Benarcos R.;  
 RT "Structure of the human lck gene: differences in genomic organisation  
 within src-related genes affect only N-terminal exons.";  
 RT Gene 84:105-113(1989).  
 RL RN [4]  
 RP NUCLEOTIDE SEQUENCE [mRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;  
 RP VAL-352 AND LEU-446, AND PHOSPHORYLATION SITES TYR-393 AND TYR-504.  
 RC TISSUE=Leukemia;  
 RX MEDLINE=94187714; PubMed=8139546;  
 RA Wright D.D., Sefton B.M., Kamps M.P.;  
 RA "Oncogenic activation of the lck protein accompanies translocation of  
 the lck gene in the human HSB2 T-cell leukemia.";  
 RL RN [5]  
 RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM SHORT), AND ALTERNATIVE SPlicing.  
 RC TISSUE=Leukemic T-cell;  
 RX MEDLINE=96085119; PubMed=7495859; DOI=10.1016/0167-4781(95)00162-A;  
 RA Vogel L.B., Arthur R., Fujita D.J.;  
 RT RT "An aberrant lck mRNA in two human T-cell lines.";  
 RL RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM 3).  
 RG Human chromosome 1 international sequencing consortium;  
 RL RN [7]  
 RP Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schueler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL RN [8]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.  
 RX MEDLINE=89096891; PubMed=2850479;  
 RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;  
 RT "Structure of the murine lck gene and its rearrangement in a murine  
 lymphoma cell line.";  
 RT Mol. Cell. Biol. 8:3058-3064 (1988).  
 RL RN [9]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.  
 RX MEDLINE=89313764; PubMed=2787474;  
 RA Takadera T., Leung S., Germone A., Koga Y., Takihara Y.,  
 RA Miyamoto N.G., Mak T.W.;  
 RT "Structure of the two promoters of the human lck gene: differential  
 accumulation of two classes of lck transcripts in T cells.";  
 RT Mol. Cell. Biol. 9:2173-2180 (1989).

RN NUCLEOTIDE SEQUENCE [mRNA].

RX MEDLINE=87133831; PubMed=3493153;

RA Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,  
 RA Mak T.W.;

RT "A human T cell-specific cDNA clone (YT16) encodes a protein with  
 extensive homology to a family of protein-tyrosine kinases.";  
 RL Eur. J. Immunol. 16:1643-1646(1986).  
 RN [2]

RN [10] NUCLEOTIDE SEQUENCE [mRNA] OF 13-508.  
 RP TISSUE=Peripheral blood lymphocyte;  
 RC MEDLINE=20462621; PubMed=11009097;  
 RX DOI=10.1002/1521-4141(200009)30:9<2632::AID-IMMU2632>3.0.CO;2-C;  
 RA Boncristiano M., Majolini M.B., D'Ellos M.M., Pacini S., Valensin S.,  
 RA Baldari C.T., Amedei A., Falini B., Del Prete G., Telford J.L.,  
 RT "Defective recruitment and activation of ZAP-70 in common variable  
 RT immunodeficiency patients with T cell defects.;"  
 RL Eur. J. Immunol. 30:2632-2638(2000).  
 RN [11] NUCLEOTIDE SEQUENCE [mRNA] OF 367-508.  
 RP MEDLINE=88217332; PubMed=2835736;  
 RA Veillette A., Foss F.M., Sauvville E.A., Bolen J.B., Rosen N.;  
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma  
 RT and other non-lymphoid human tumor cell lines.;"  
 RL Oncogene Res. 1:357-374(1987).  
 RN [12] NUCLEOTIDE SEQUENCE [mRNA] OF 374-508.  
 RP MEDLINE=87000726; PubMed=3489486; DOI=10.1016/0167-4889(86)90228-4;  
 RX Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,  
 RA Linna T.J.;  
 RT "Human T lymphocytes express a protein-tyrosine kinase homologous to  
 RT p56LSTRA."  
 RL Biochim. Biophys. Acta 888:286-295 (1986).  
 RN [13] PHOSPHORYLATION SITE TYR-504.  
 RP MEDLINE=923347326; PubMed=16339064;  
 RX Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,  
 RA Amrein K.E., Autero M., Burn P., Alitalo K.;  
 RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and  
 down regulates its catalytic activity.;"  
 RL EMBO J. 11:2919-2924(1992).  
 RN [14] INTERACTION WITH PI3K.  
 RP MEDLINE=94067101; PubMed=7504174;  
 RX Vogel L.B., Fujita D.J.;  
 RT "The SH3 domain of p56lck is involved in binding to  
 phosphatidylinositol 3'-kinase from T lymphocytes.;"  
 RL Mol. Cell. Biol. 13:7408-7417(1993).  
 RN [15] INTERACTION WITH KDRBS1.  
 RP MEDLINE=95155308; PubMed=7852312; DOI=10.1074/jbc.270.6.2506;  
 RA Vogel L.B., Fujita D.J.;  
 RT "p70 phosphorylation and binding to p56lck is an early event in  
 inter-leukin-2-induced onset of cell cycle progression in T-  
 lymphocytes.";  
 RL J. Biol. Chem. 270:2506-2511(1995).  
 RN [16] INTERACTION WITH SQSTM1, AND MUTAGENESIS OF SER-58 AND ARG-153.  
 RP PubMed=8618896;  
 RA Park I., Chung J., Walsh C.T., Yun Y., Strominger J.L., Shin J.;  
 RT "Phosphotyrosine-independent binding of a 62-kDa protein to the src  
 homology 2 (SH2) domain of p56lck and its regulation by  
 phosphorylation of Ser-59 in the lck unique N-terminal region.;"  
 RT Proc. Natl. Acad. Sci. U.S.A. 92:12338-12342(1995).  
 RN [17] INTERACTION WITH HIV-1 NEF.  
 RP MEDLINE=96386556; PubMed=8794306;  
 RA Greenway A.L., Azad A., Mills J., McPhee D.A.;  
 RT "Human immunodeficiency virus type 1 Nef binds directly to LCK and  
 mitogen-activated protein kinase, inhibiting kinase activity.;"  
 RL J. Virol. 70:6701-6708(1996).  
 RN [18] REVIEW.  
 RP PubMed=10848956;  
 RA Isakov N., Biesinger B.;  
 RT "Lck protein tyrosine kinase is a key regulator of T-cell activation  
 and a target for signal intervention by Herpesvirus saimiri and other  
 viral gene products.";  
 RL Eur. J. Biochem. 267:3413-3421(2000).  
 RN [19]

RN [10] SUBCELLULAR LOCATION.  
 RP TISSUE=Mammary cancer;  
 RX PubMed=12218089;  
 RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,  
 RA Minaki Y., Kato A., Tani-Ichi S., Hamada T., Kosugi A.;  
 RT "Fyn is essential for tyrosine phosphorylation of Csk-binding  
 protein/phosphoprotein associated with glycolipid-enriched  
 microdomains in lipid rafts in resting T cells.";  
 RT J. Immunol. 169:2813-2817(2002).  
 RL [20] MASS SPECTROMETRY.  
 RP TISSUE=Mammary cancer;  
 RX PubMed=21829512; PubMed=11840567;  
 RX DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;  
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,  
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,  
 RA Zvelebil M.J.;  
 RT "Cluster analysis of an extensive human breast cancer cell line  
 protein expression map database.;"  
 RT RL Proteomics 2:212-223(2002).  
 RN [21] INTERACTION WITH LIME1.  
 RP PubMed=14610046; DOI=10.1084/jem.20031484;  
 RX Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,  
 RA Hilgert I., Paces J., Simeoni L., Klische S., Merten C., Schraven B.,  
 RA Horejsi V.;  
 RT "LIME: a new membrane raft-associated adaptor protein involved in CD4  
 and CD8 coreceptor signaling.;"  
 RL J. Exp. Med. 198:1453-1462(2003).  
 RN [22] INTERACTION WITH LIME1.

Query Match 100.0%; Score 51; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 1,1;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 DYLRVSLED <span style="color:red">F</span> 10
Db	487 DYLR <span style="color:red">S</span> LED <span style="color:red">F</span> 496

RESULT 4  
 LCK\_SAISC  
 ID LCK\_SAISC STANDARD; PRT; 508 AA.  
 AC Q95KR7;  
 DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 07-MAR-2006, entry version 26;  
 DE Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (p56-LCK)  
 DE (Lymphocyte cell-specific protein-tyrosine kinase).  
 GN Name=LCK;  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;  
 OC Cebinae; Saimiri.  
 OX NCBI\_TaxID=9521;  
 RN [1] NUCLEOTIDE SEQUENCE [mRNA], ENZYME REGULATION, AND INTERACTION WITH  
 RP SAIMIRINE HERPESVIRUS 2 TIP.  
 RC TISSUE=T-cell;  
 RX MEDLINE=21424508; PubMed=11533187;  
 RX DOI=10.1128/JVI.75.19.9252-9261.2001;  
 RA Greve T., Tamgouney G., Fleischner H., Broeker B.M.;  
 RT "Downregulation of p56lck tyrosine kinase activity in T cells of  
 squirrel monkeys (Saimiri sciureus) correlates with the non-  
 transforming and apathogenic properties of herpesvirus saimiri in its  
 natural host.;"  
 RT J. Virol. 75:9252-9261(2001).  
 RL CC -!- FUNCTION: Tyrosine kinase that plays an essential role for the  
 selection and maturation of developing T-cell in the thymus and in  
 mature T-cell function. Is constitutively associated with the  
 cytoplasmic portions of the CD4 and CD8 surface receptors and  
 plays a key role in T-cell antigen receptor(TCR)-linked signal  
 transduction pathways. Association of the TCR with a peptide

CC antigen-bound MHC complex facilitates the interaction of CD4 and CC CD8 with MHC class II and class I molecules, respectively, and CC thereby recruits the associated LCK to the vicinity of the TCR/CD3 complex. LCK then phosphorylates tyrosines residues within the CC immunoreceptor tyrosines-based activation motifs (ITAMs) in the CC cytoplasmic tails of the TCRgamma chains and CD3 subunits, CC initiating the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with CC the cytoplasmic tail of CD2, and upon engagement of the CD2 molecule, LCK undergoes hyperphosphorylation and activation. Also CC plays a role in the IL2 receptor-linked signaling pathway that CC controls T-cell proliferative response. Binding of IL2 to its receptor results in increased activity of LCK. Is expressed at all CC stages of thymocyte development and is required for the regulation CC of maturation events that are governed by both pre-TCR and mature CC alpha beta TCR (By similarity). CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein CC tyrosine phosphate. CC -!- ENZYME REGULATION: Regulated by phosphatases. CC -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface CC receptors, such as CD2, CD4, CD8, CD44, CD45 and CD122. Also CC binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to CC other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds CC to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes CC through its SH3 domain and to the tyrosine phosphorylated form of CC KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1. CC Interacts with phosphorylated LIME1. Interacts with CBLB (By CC similarity). Interacts with sainirine herpesvirus 2 TIP. CC -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane. CC -!- Present in lipid rafts in an unactive form (By similarity). CC -!- TISSUE SPECIFICITY: Expressed specifically in lymphoid cells. CC -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout CC T-cell ontogeny. CC -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1. CC Interaction is regulated by Ser-58 phosphorylation (By CC similarity). CC -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This CC phosphorylation downregulates catalytic activity. Phosphorylated CC on Tyr-393 either by itself or another kinase, leading to CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. CC -!- SIMILARITY: Contains 1 SH2 domain. CC -!- SIMILARITY: Contains 1 SH3 domain. CC -!- CAUTION: LCK seems to be active in all vertebrates, except in squirrel monkey T-cells, in which it is inactivated. The reason seems to be that squirrel monkey are the natural host for Sainirine herpesvirus 2, which is able to efficiently transform T-cells through a mechanism involving viral Tip/ host LCK interaction. Its inactivation may a mechanism that specifically counteracts the transformation effects of viral Tip.

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 EMBL: AU277921; CAC38871.1; - ; mRNA.  
 DR HSSP; P06239; 1LKK.  
 DR SMR; Q95KR7; 64-508.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF007714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 SMART; SM00252; SH2; 1.

DR	SMART; SM00326; SH3; 1.	
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DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	
DR	PROSITE; PS50001; SH2; 1.	
DR	PROSITE; PS50002; SH3; 1.	
KW	ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.	
KW	INIT_MET	
FT	CHAIN	
FT	DOMAIN	
FT	60	120
FT	126	223
FT	244	497
FT	250	258
FT	1	71
FT	NP_BIND	
FT	REGION	
FT	ACT_SITE	
FT	363	363
FT	BINDING	
FT	272	272
FT	MOD_RES	
FT	393	393
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FT		5088C64061853819 CRC64;
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FT	1	DYLRSVLEDF 10
FT	Db	
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Query Match Best Local Similarity 100.0%; Score 51; DB 1; Length 508; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RX	MEDLINE=22289034; PubMed=12401726;	
RA	Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D.,	
RA	Naquet P., Matsuda F., Imbert J., Vialettes B.;	
RT	"No association between lck gene polymorphisms and protein level in type 1 diabetes." Diabetes 51:3326-3330 (2002).	
RT	Diabetes 51:3326-3330 (2002).	
RL	-!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.	
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a> Distributed under the Creative Commons Attribution-NoDerivs License	
CC	EMBL; BN000073; CAD55807.1; - ; Genomic_DNA.	
CC	PRINTS; PR00401; SH2DOMAIN.	
CC	PRINTS; PR00452; SH3DOMAIN.	
CC	PRINTS; PR00109; TYRKINASE.	
CC	ProDom; PD000001; Prot_kinase; 1.	
CC	ProDom; PD000093; SH2; 1.	
CC	ProDom; PD000066; SH3; 1.	
CC	SMART; SM00252; SH2; 1.	
DR	SMART; SM00326; SH3; 1.	
DR	PROSITE; PS00219; TyrKC; 1.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	
DR	PROSITE; PS50001; SH2; 1.	
DR	PROSITE; PS50002; SH3; 1.	
DR	ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.	
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DR GO; GO:0000242; C:pericentriolar material; ISS.  
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.  
 DR GO; GO:0042169; F:SH2 domain binding; ISS.  
 DR GO; GO:0006919; P:caspase activation; ISS.  
 DR GO; GO:0030097; P:hemopoiesis; ISS.  
 DR GO; GO:0006917; P:induction of apoptosis; ISS.  
 DR GO; GO:0007242; P:intracellular signaling cascade; ISS.  
 DR GO; GO:00050870; P:positive regulation of T cell receptor sign. . . ; ISS.  
 DR GO; GO:0050862; P:positive regulation of T cell receptor sign. . . ; ISS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.  
 DR GO; GO:0007265; P:Ras protein signal transduction; ISS.  
 DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.  
 DR GO; GO:0000074; P:regulation of progression through cell cycle; ISS.  
 DR GO; GO:0042493; P:response to drug; ISS.  
 DR GO; GO:0030217; P:T cell differentiation; ISS.  
 DR GO; GO:0006882; P:zinc ion homeostasis; ISS.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODom; PD000001; Prot\_kinase; 1.  
 DR PRODom; PD000093; SH2; 1.  
 DR PRODom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW SEQUENCE 509 AA; 58001 MW; 44BFF0D43FFB420D CRC64;

Query Match 100.0%; Score 51; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLED 10  
 Db 488 DYLRSVLED 497

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RESULT 6

Q95M32\_9PRIM PRELIMINARY; PRT; 509 AA.

ID Q95M32\_9PRIM PRELIMINARY; PRT; 509 AA.

AC Q95M32; 01-DEC-2001, integrated into UniProtKB/TREMBL.  
 DT 01-DEC-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 18.

DB Lck protein.  
 GN Name=Lck;  
 OS Hylobates sp. (gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=9581;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;  
 RA Picard C., Greenway A., Holloway G., Olive D., Collette Y.;  
 "Interaction with simian Hck tyrosine kinase reveals convergent evolution of the Nef protein from simian and human immunodeficiency viruses despite differential molecular surface usage.";

RL Virology 295:320-327 (2002).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Picard C.; Thesis (2001), Department of Experimental Oncology laboratory, U. Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

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CC EMBL; AJ320182; CAC44027.1; -; mRNA.

CC HSSP; P06239; 1LCK.

DR DR SMR; Q95M32; 65-509.

DR DR GO; GO:0045121; C:lipid raft; ISS.

DR DR GO; GO:0000242; C:pericentriolar material; ISS.

DR DR GO; GO:0000242; F:protein serine/threonine phosphatase activity; ISS.

DR DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.

DR DR GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

DR DR GO; GO:0042169; F:SH2 domain binding; ISS.

DR DR GO; GO:0006919; P:caspase activation; ISS.

DR DR GO; GO:00030097; P:hemopoiesis; ISS.

DR DR GO; GO:0006917; P:induction of apoptosis; ISS.

DR DR GO; GO:0007242; P:intracellular signaling cascade; ISS.

DR DR GO; GO:0050870; P:positive regulation of T cell receptor sign. . . ; ISS.

DR DR GO; GO:0050862; P:positive regulation of T cell receptor sign. . . ; ISS.

DR DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

DR DR GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

DR DR GO; GO:0042169; F:SH2 domain binding; ISS.

DR DR GO; GO:0006919; P:caspase activation; ISS.

DR DR GO; GO:00030097; P:hemopoiesis; ISS.

DR DR GO; GO:0006917; P:induction of apoptosis; ISS.

DR DR GO; GO:0007265; P:Ras protein signal transduction; ISS.

DR DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.

DR DR GO; GO:0000074; P:regulation of progression through cell cycle; ISS.

DR DR GO; GO:0042493; P:response to drug; ISS.

DR DR GO; GO:0030217; P:T cell differentiation; ISS.

DR DR GO; GO:0006882; P:zinc ion homeostasis; ISS.

DR DR InterPro; IPR00719; Prot\_kinase.

DR DR InterPro; IPR002290; Ser\_thr\_pk kinase.

DR DR InterPro; IPR000980; SH2.

DR DR InterPro; IPR001452; SH3.

DR DR InterPro; IPR001245; Tyr\_pk kinase.

DR DR InterPro; IPR008266; Tyr\_pk kinase\_AS.

DR DR Pfam; PF00714; Pkinase\_Tyr; 1.

DR DR Pfam; PF00018; SH3\_1; 1.

DR DR PRINTS; PR00401; SH2DOMAIN.

DR DR PRINTS; PR00452; SH3DOMAIN.

DR DR PRINTS; PR00109; TYRKINASE.

DR DR PRODom; PD000001; Prot\_kinase; 1.

DR DR PRODom; PD000093; SH2; 1.

DR DR PRODom; PD000066; SH3; 1.

DR DR SMART; SM00252; SH2; 1.

DR DR SMART; SM00326; SH3; 1.

DR DR SMART; SM00219; TYRK; 1.

DR DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR DR PROSITE; PS50001; SH2; 1.

DR DR PROSITE; PS50002; SH3; 1.

DR DR SEQUENCE 509 AA; 57947 MW; F1BF5C237C8DB7E CRC64;

Query Match 100.0%; Score 51; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLED 10  
 Db 488 DYLRSVLED 497

---

RESULT 7

O3ZCM0\_BOVIN PRELIMINARY; PRT; 509 AA.

ID Q3ZCM0\_BOVIN PRELIMINARY; PRT; 509 AA.

AC Q3ZCM0;

DT 27-SEP-2005, integrated into UniProtKB/TREMBL.

DT 27-SEP-2005, sequence version 1.

DT 07-MAR-2006, entry version 6.

DE Hypothetical protein MGCI26900.

GN Name=MGCI26900;

OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Crossbred x Angus; TISSUE=Ileum;  
 RA Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,  
 RA Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,  
 RA Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,  
 RA Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,  
 RA Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,  
 RA Siddiqui A., Holt R., Jones S.J., Marra M.A.;  
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
 CC  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 EMBL; BC102046; AA102047.1; -; mRNA.  
 DR GO; GO:0045121; C:lipid raft; ISS.  
 DR GO; GO:000242; C:pericentriolar material; ISS.  
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.  
 DR GO; GO:0042169; F:SH2 domain binding; ISS.  
 DR GO; GO:0003097; P:caspase activation; ISS.  
 DR GO; GO:0006919; P:hemopoiesis; ISS.  
 DR GO; GO:0006917; P:induction of apoptosis; ISS.  
 DR GO; GO:0007242; P:intracellular signaling cascade; ISS.  
 DR GO; GO:0050870; P:positive regulation of T cell activation; ISS.  
 DR GO; GO:0050862; P:positive regulation of T cell receptor sign. . . ; ISS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.  
 DR GO; GO:007265; P:Ras protein signal transduction; ISS.  
 DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.  
 DR GO; GO:0000074; P:regulation of progression through cell cycle; ISS.  
 DR GO; GO:0042493; P:response to drug; ISS.  
 DR GO; GO:0030217; P:T cell differentiation; ISS.  
 DR GO; GO:0006882; P:zinc ion homeostasis; ISS.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Prints; PR00401; SH2DOMAIN.  
 DR Prints; PR00452; SH3DOMAIN.  
 DR Prints; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 509 AA; 5833 MW; CE0E80DCD6D0F2F8 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLED 10  
 Db 488 DYLRSVLED 497

RESULT 8  
 Q573B4\_HUMAN PRELIMINARY; PRT; 516 AA.  
 ID Q573B4\_HUMAN AC  
 AC Q573B4;  
 DT 10-MAY-2005, integrated into UniProtKB/Trembl.  
 DT 10-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE Proto-oncogene tyrosine-protein kinase LCK.  
 GN Name=LCK;  
 RA Homo sapiens (Human).  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Cetartiodactyla; Ruminantia;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Blood;  
 RX PubMed=16107303; DOI=10.1016/j.gene.2005.06.018;  
 RA Nervi S., Guinamard R., Delaval B., Lecine P., Vialettes B.,  
 RA Naquet P., Imbert J.;  
 RA "A rare mRNA variant of the human lymphocyte-specific protein tyrosine kinaseLCK gene with intron B retention and exon 7 skipping encodes a putativeprotein with altered SH3-dependent molecular interactions.";  
 RL Gene 359:18-25 (2005).  
 CC  
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 EMBL; AJ865079; CAI23831.1; -; mRNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Prints; PR00401; SH2DOMAIN.  
 DR Prints; PR00452; SH3DOMAIN.  
 DR Prints; PR00109; TYRKINASE.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Kinase.  
 SQ SEQUENCE 516 AA; 5833 MW; EB9A52D4EBDF14D2 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSVLED 10  
 Db 495 DYLRSVLED 504

RESULT 9  
 Q9U8V6\_EPTBU ID Q9U8V6\_EPTBU PRELIMINARY; PRT; 249 AA.  
 AC Q9U8V6;  
 DT 01-MAY-2000, integrated into UniProtKB/Trembl.  
 DT 01-MAY-2000, sequence version 1.  
 DT 07-FEB-2006, entry version 28.  
 DE Src-like A (Fragment).  
 OS Eptatretus burgeri (Inshore hagfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;  
 OC Myxinidae; Eptatretinae; Eptatretus.  
 OX NCBI\_TaxID=7764;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE  
 RX MEDLINE=20020330; PubMed=10552041; SUGA H., Hoshiyama D., Kuraku S., Katoh K., Kubokawa K., Miyata T.;  
 RA "Protein tyrosine kinase cDNAs from amphioxus, hagfish, and lamprey:  
 RT isoform duplications around the divergence of cyclostomes and gnathostomes.";  
 RT J. Mol. Evol. 49:601-608(1999).  
 RL -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

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CC CC

CC EMBL; AB025546; BAA84736.1; -; mRNA.  
 DR HSSP; P06239; 1OPC.  
 DR SMR; Q9U8V6; 1-249.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_Pkinase.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR KW Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 249 AA; 28636 MW; D7F37EE197EA580C CRC64;

Query Match 94.1%; Score 48; DB 2; Length 249;  
 Best Local Similarity 90.0%; Pred. No. 1.9;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYLRSLVLED 10  
 Db 228 DYLKSVLED 237

RESULT 10

Q3TLX4\_MOUSE PRELIMINARY; PRT; 368 AA.  
 AC Q3TLX4;  
 DT 11-OCT-2005, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 7.  
 DE Mammary gland RCB-0526 JYG-MC(A) cDNA, RIKEN full-length enriched library, clone:G830026006 product:lymphocyte protein tyrosine kinase, full insert sequence. (Fragment).  
 DE Name=Lick;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE  
 RN TISSUE=Mammary gland;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RT Methods Enzymol. 303:19-44(1999).  
 RL [2]  
 RP NUCLEOTIDE SEQUENCE  
 RC TISSUE=Mammary gland;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Battalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impiombato A., Apweiler R., Attaraliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Garibaldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Humminck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuura S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Komo H., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watanahiki A., Okamura-Ohno Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.",  
 RL Science 309:1559-1563 (2005).  
 RN [3]

RP TISSUE=Mammary gland;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 RT (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566 (2005).  
 RN [4]

RP NUCLEOTIDE SEQUENCE  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Battalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai J.H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [5]

RC NUCLEOTIDE SEQUENCE;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Built C., Fletcher C., Fujita M., Garibaldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [6]

RC NUCLEOTIDE SEQUENCE;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Carninci P., Shibata K., Nagaoaka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [7]

RC NUCLEOTIDE SEQUENCE;  
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [8]

RC NUCLEOTIDE SEQUENCE;  
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [8]

RC NUCLEOTIDE SEQUENCE;  
 TISSUE=Mammary gland;  
 RC MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsubara S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [8]

RESULT 11

Q4FZR6	RAT	PRELIMINARY;	PRT;	379 AA.
Q4FZR6	RAT			
AC				
DT				
DT				
DE				
GN				
OS				
OC				
OX				
RN				
RP				

Query Match 94.1%; Score 48; DB 2; Length 368;  
 Best Local Similarity 90.0%; Pred. No. 2.9;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLEDFF 10  
 Db 347 DYLRSVLDFF 356

DR InterPro; IPRO00719; Prot\_kinase.  
 DR InterPro; IPRO02290; Ser\_thr\_Pkinase.  
 DR InterPro; IPRO00980; SH2.  
 DR InterPro; IPRO01245; Tyr\_Pkinase.  
 DR InterPro; IPRO08266; Tyr\_Pkinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD00001; Prot\_kinase; 1.  
 DR ProDom; PD00093; SH2; 1.  
 DR SMART; SM00219; TyrK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding; Transferase;  
 KW Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 368 AA; 42018 MW; 7AB6A53AFIA5059 CRC64;

NCBI\_TaxID=10116;

[1]

RC NUCLEOTIDE SEQUENCE;  
 TISSUE=Thymus;  
 RC MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefter C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., de Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA and mouse cDNA sequences.";  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]

CC NUCLEOTIDE SEQUENCE.  
 CC Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.

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 DR EMBL; AK166263; BAE38668.1; -; mRNA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; RCA.  
 DR NIH MGC Project;  
 RL Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

CC  
RN Nature 319:682-685(1986).

CC  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].

CC  
[3] STRAIN=NOD; TISSUE=Thymus;

CC  
RX PubMed=16141072; DOI=10.1126/science.1112014;

CC  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
Bajic V.B., Brenner S.E., Battalov S., Forrest A.R., Zavolan M.,  
Davis M.J., Wilming L.G., Aiddinis V., Allen J.E.,  
Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
Fletcher C.F., Fukushina T., Furuno M., Futaki S., Gariboldi M.,  
Goracci-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirakawa N.,  
InterPro; IPR001245; Tyr\_pk kinase.

CC  
DR InterPro; IPR000719; Prot kinase.

CC  
DR InterPro; IPR0008266; Tyr\_pk kinase\_AS.

CC  
DR InterPro; IPR0008266; Tyr\_pk kinase\_TS.

CC  
DR InterPro; IPR00017; SH2; 1.

CC  
DR PRINTS; PR00401; SH2DOMAIN.

CC  
DR PRINTS; PR00109; TYRKINASE.

CC  
DR PRODom; PD00001; Prot\_kinase; 1.

CC  
DR PRODom; PD000093; SH2; 1.

CC  
DR SMART; SM00252; SH2; 1.

CC  
DR SMART; SM00219; TYRKc; 1.

CC  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

CC  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

CC  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

CC  
DR PROSITE; PS50001; SH2; 1.

CC  
KW ATP-binding; Kinase; Nucleotide-binding; Transferase;  
KW Tyrosine-protein kinase.

CC  
FT NON\_TER 1 1

CC  
SQ SEQUENCE 379 AA; 43336 MW; 7CDEB573BAFB53AB CRC64;

CC  
Query Match 94.1%; Score 48; DB 2; Length 379;

CC  
Best Local Similarity 90.0%; Pred. No. 3;

CC  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC  
QY 1 DYLRSVLEDF 10

CC  
Db 358 DYLRSVLDDF 367

CC  
RN RESULT 12

CC  
LCK\_MOUSE ID LCK\_MOUSE STANDARD; PRT; 508 AA.

CC  
AC P06240; Q61794; Q62320; Q91X65;

CC  
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.

CC  
DT 25-OCT-2005, sequence version 3.

CC  
DT 07-MAR-2006, entry version 74.

CC  
DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)

CC  
DE (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).

CC  
GN Name=Lck; Synonyms=Lsk-t;

CC  
OS Mus musculus (Mouse)

CC  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

CC  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

CC  
OC Muroidea; Muridae; Murinae; Mus.

CC  
NCBI\_TaxID=10090;

CC  
RN [1] NUCLEOTIDE SEQUENCE [mRNA].

CC  
RN MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;

CC  
RA Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;  
"A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpressed in the murine T cell lymphoma LSTRA."; retrovirus promoter insertion.";

CC  
RN [2] NUCLEOTIDE SEQUENCE [mRNA].

CC  
RN MEDLINE=86146842; PubMed=3081813;

CC  
RA Voronova A.F., Sefton B.M.;  
"Expression of a new tyrosine protein kinase is stimulated by

CC  
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.

CC  
RN MEDLINE=89096891; PubMed=2850479;

CC  
RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;  
"Structure of the murine lck gene and its rearrangement in a murine

CC  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC  
RN [5] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.

RT Lymphoma cell line.";  
 RL Mol. Cell. Biol. 8:3058-3064 (1988).  
 RN [6]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.  
 RX MEDLINE=88142832; PubMed=3501824;  
 RA Voronova A.F., Adler H.T., Sefton B.M.;  
 RT "Two lck transcripts containing different 5' untranslated regions are  
 present in T cells.";  
 RL Mol. Cell. Biol. 7:4407-4413 (1987).  
 RN [7]

RP MUTAGENESIS OF TYR-504.  
 RX MEDLINE=88248001; PubMed=3380790;  
 RA Amrein K.E., Sefton B.M.;  
 RT "Avian reovirus mRNAs are nonfunctional in infected mouse cells:  
 translational basis for virus host-range restriction.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261 (1988).  
 RN [8]

RP INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19  
 AND CYS-22.  
 RX MEDLINE=90182655; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;  
 RA Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,  
 RA Littman D.R.;  
 RT "Interaction of the unique N-terminal region of tyrosine kinase p56lck  
 with cytoplasmic domains of CD4 and CD8 is mediated by cysteine  
 motifs.";  
 RL Cell 60:755-765 (1990).  
 RN [9]

RP MUTAGENESIS.  
 RX MEDLINE=93059694; PubMed=1279202;  
 RA Hurley T.R., Amrein K.E., Sefton B.M.;  
 RT "Creation and characterization of temperature-sensitive mutants of the  
 lck tyrosine protein kinase.";  
 RL J. virol. 66:7406-7413 (1992).  
 RN [10]

RP MUTAGENESIS OF LYS-272.  
 RX MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;  
 RA Abraham N., Miceli M.C., Parnes J.C., Veillette A.;  
 RT "Enhancement of T-cell responsiveness by the lymphocyte-specific  
 tyrosine protein kinase p56lck.";  
 RL Nature 350:62-66 (1991).  
 RN [11]

RP MUTAGENESIS OF TYR-504.  
 RX MEDLINE=91219495; PubMed=1708890;  
 RA Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;  
 RT "Thymic tumorigenesis induced by overexpression of p56lck.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981 (1991).  
 RN [12]

RP PHOSPHORYLATION BY CSK.  
 RX PubMed=8371758; DOI=10.1038/365156a0;  
 RA Chow I.M., Fournel M., Davidson D., Veillette A.;  
 RT "Negative regulation of T-cell receptor signalling by tyrosine protein  
 kinase p50csk.";  
 RL Nature 365:156-160 (1993).  
 RN [13]

RP MUTAGENESIS.  
 RX MEDLINE=93133805; PubMed=8421674;  
 RA Carrera A.C., Alexandrov K., Roberts T.M.;  
 RT "The conserved lysine of the catalytic domain of protein kinases is  
 actively involved in the phosphotransfer reaction and not required for  
 anchoring ATP.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:442-446 (1993).  
 RN [14]

RP PALMITOYLATION.  
 RX MEDLINE=94019312; PubMed=8413237;  
 RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;  
 RT "Palmitylation of an amino-terminal cysteine motif of protein tyrosine  
 kinases p56lck and p59fyn mediates interaction with glycosyl-  
 phosphatidylinositol-anchored proteins.";  
 RL Mol. Cell. Biol. 13:6385-6392 (1993).  
 RN [15]

RP PALMITOYLATION.  
 RX MEDLINE=95071286; PubMed=7980442;  
 RA Koegl M., Zlatkine P., Ley S.C., Courtney S.A., Magee A.I.;

RT "Palmitylation of multiple Src-family kinases at a homologous N-  
 terminal motif.";  
 RT Biochem. J. 303:749-753 (1994).  
 RL [16]

RP INTERACTION WITH CBLB.  
 RX PubMed=10646608; DOI=10.1038/35003228;  
 RA Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,  
 RA Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,  
 RA Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,  
 RA Penninger J.M.;  
 RT "Negative regulation of lymphocyte activation and autoimmunity by the  
 molecular adaptor Cbl-b.";  
 RL Nature 403:211-216 (2000).  
 RN [17]

RP SUBCELLULAR LOCATION.  
 RX PubMed=12218089;  
 RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,  
 RA Minaki Y., Katto A., Tani-Ichi S., Hamaoka T., Kosugi A.;  
 RT "Fyn is essential for tyrosine phosphorylation of Csk-binding  
 protein/phosphoprotein associated with glycolipid-enriched  
 microdomains in lipid rafts in resting T cells.";  
 RL J. Immunol. 169:2813-2817 (2002).  
 RN [18]

RP PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.  
 RX PubMed=15592455; DOI=10.1038/nbt1046;  
 RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,  
 RA Zha X.-M., Polakiewicz R.D., Comb M.J.;  
 RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer

Qy	1	DYLRSVLEDFF 10
Db	487	DYLRSVLDFF 496

Query Match 94.1%; Score 48; DB 1; Length 508;  
 Best Local Similarity 90.0%; Pred. No. 4,1;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
 Q4RNX3\_TETNG  
 ID Q4RNX3\_TETNG PRELIMINARY; PRT; 466 AA.  
 AC Q4RNX3;  
 DT 19-JUL-2005, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 5.  
 DE Chromosome 10 SCAF1509, whole genome shotgun sequence. (Fragment).  
 GN ORFNames=GSTENG00031368001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleosteii;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetradontoidea; Tetraodontidae; Tetraodon.  
 NCBI\_TaxID=99883;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15496914; DOI=10.1038/nature03025;  
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicuda S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Basilia C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,  
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Vollff J.-N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quettier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957 (2004).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell  
 cycle. It is required in higher cells for entry into S-phase and  
 mitosis. Component of the kinase complex that phosphorylates the  
 repetitive C-terminus of RNA polymerase II. Catalytic component of  
 MPP (BY similarity).  
 CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
 mature oocytes (BY similarity).  
 CC -!- SIMILARITY: Contains 1 SH3 domain.

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 CC  
 EMBL; CAAE01015009; CAG09909.1; -; Genomic\_DNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:000166; F:nucleotide binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_Pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00018; SH2; 1.  
 DR Prints; PR00452; SH3DOMAIN.  
 DR Prints; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK\_C; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 DR Kinase.  
 KW ATP-binding; Kinase; Nucleotide-binding; SH3 domain; Transferase.  
 FT SEQUENCE 466 AA; 53437 MW; E35D93F87395B799 CRC64;

---

Query Match 92.2%; Score 47; DB 2; Length 466;  
 Best local Similarity 90.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLED 10  
 Db 448 EYLRSVLED 457

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RESULT 14  
 OI3064\_XENLA ID OI3064\_XENLA PRELIMINARY; PRT; 488 AA.  
 AC 013064; DT 01-JUL-1997, integrated into UniProtKB/TREMBL.  
 DT 01-JUL-1997, sequence version 1.  
 DT 07-FEB-2006, entry version 29.  
 DE Lyn protein tyrosine kinase.  
 GN Name=Lyn;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 NCBI\_TaxID=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Fukami Y., Funabiki K., Sato K.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

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 CC  
 EMBL; AB003358; BAA20078.1; -; mRNA.  
 DR SMR; O13064; 43-488.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_Pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR Pfam; PF00018; Pkinase\_Tyr; 1.  
 DR Prints; PR00452; SH3DOMAIN.  
 DR Prints; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK\_C; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 DR Kinase.  
 KW SEQUENCE 488 AA; 55795 MW; B7E70668B6EA92B2 CRC64;

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Query Match 86.3%; Score 44; DB 2; Length 488;  
 Best local Similarity 80.0%; Pred. No. 22; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYLRSVLED 10  
 Db 467 DYLOSVLDDF 476

---

RESULT 15  
 Q3U6Q5\_MOUSE ID Q3U6Q5\_MOUSE PRELIMINARY; PRT; 491 AA.  
 AC Q3U6Q5; DT 11-OCT-2005, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, sequence version 5.  
 DE Bone marrow macrophage cDNA, RIKEN full-length enriched library,  
 DE clone:1830119M13 product:Yamaguchi sarcoma viral (v-yes-1) oncogene  
 DE homolog, full insert sequence.  
 DE Name=Lyn;  
 OS Mus musculus (Mouse).  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
 RX MEDLINE=9927925; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RT Methods Enzymol. 303:19-44 (1999).  
 RL  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., RA  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., RA  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., RA  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E., RA  
 RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., RA  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., RA  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., RA  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., RA  
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., RA  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., RA  
 RA Georgii-Hemming P., Gingera T.R., Gojobori T., Green R.E., RA  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., RA  
 RA Hill D., Hummiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., RA  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., RA  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., RA  
 RA Kurochkin I.V., Larneau L.F., Lazarevic D., Lipovich L., Liu J., RA  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., RA  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., RA  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., RA  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., RA  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., RA  
 RA Petrovsky N., Piazza S., Reid J.F., Ring B.Z., Ringwald M., RA  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., RA  
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., RA  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., RA  
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K., RA  
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., RA  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., RA  
 RA Yamamoto H., Zaborsky E., Zhu S., Zimmer A., Hide W., Bult C., RA  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., RA  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., RA  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., RA  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., RA  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., RA  
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., RA  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., RA  
 RA Hayashizaki Y.; "The transcriptional landscape of the mammalian genome."; RT  
 RT Science 309:1559-1563 (2005). RT  
 RN [13]

RL NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone marrow; RT  
 RX PubMed=16141073; DOI=10.1126/science.1112009; RT  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group RT  
 RG (Genome Network Core Team) and the FANTOM Consortium; RT  
 RT "Antisense Transcription in the Mammalian Transcriptome."; RT  
 RL Science 309:1564-1566 (2005). RL

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone marrow; RT  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266; RT  
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., RA  
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., RA  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishime T., Harada A., RA  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., RA  
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., RA  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RA  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RA  
 RA "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; RA  
 RA Genome Res. 10:1757-1771(2000). RA

RN [8]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Bone marrow; RT  
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., RA  
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., RA  
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., RA  
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., RA  
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., RA  
 RA Muramatsu M., Hayashizaki Y.; Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases. RA

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DR EMBL; AK153038; BAE31669.1; mRNA. DR  
 MG1; MGI:96892; Lyn. DR  
 GO; GO:0005515; F:protein binding; IPI. DR  
 GO; GO:0004713; F:protein-tirosine kinase activity; IDA. DR  
 GO; GO:0007242; P:intracellular signaling cascade; IDA. DR

DR GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.  
 DR GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.  
 DR GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.  
 DR InterPro; IPR00719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR00980; SH2.  
 DR InterPro; IPR01452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD00001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 DR SEQUENCE; 491 AA; 56285 MW; 2C82015D510B1F59 CRC64;

Query Match 86.3%; Score 44; DB 2; Length 491;  
 Best Local Similarity 80.0%; Pred. No. 22;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYLRSLVLEDF 10  
 Db 470 DYLOQSVLDDF 479

RESULT 16

Q8CEI0\_MOUSE PRELIMINARY; PRT; 491 AA.

ID Q8CEI0\_MOUSE PRELIMINARY; PRT; 491 AA.

AC Q8CEI0;

DT 01-MAR-2003, integrated into UniProtKB/TREMBL.

DT 01-MAR-2003, sequence version 1.

DT 07-FEB-2006, entry version 21.

DE 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:181073A02 product:Yamaguchi sarcoma viral homolog, full insert sequence.

GN Name=Lynn;  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

RN NCBI\_TAXID=10090;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RX Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka T., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragni T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmold S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawashima T., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Konno H., Nakamura M., Sakazume N., Sato K., Miyazaki A., Sakai K., Sasaki D., Aizawa K., Arakawa T., Fukuda S., Harada A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Yoshino M., Waterston R., Lander E.S., Rogers J., Yasunishi A., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; Nature 420:563-573 (2002). [5]

RN NUCLEOTIDE SEQUENCE.

RN Fletcher C.F., Fukushima T., Furuno M., Futaki S., Garibaldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Humanniecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuura S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Sero S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiyra K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegnér J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamamoto H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.; "The transcriptional landscape of the mammalian genome"; Science 309:1559-1563 (2005). [3]

RN RN RP RC RC RX RG RT RT RL RN RN RP RP RC RX RX RG RG RT RT RL RN RN RP NUCLEOTIDE SEQUENCE.

RT STRAIN=C57BL/6J; TISSUE=Pancreas; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome"; Science 309:1564-1566 (2005). [4]

RT RN RP NUCLEOTIDE SEQUENCE.

RT STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning"; Methods Enzymol. 303:19-44 (1999). [2]

RT NUCLEOTIDE SEQUENCE.

RT STRAIN=C57BL/6J; TISSUE=Pancreas; PubMed=16141072; DOI=10.1126/science.1112014; Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bjelic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,

RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Built C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [6]

RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [7]

RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishime T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RT Genome Res. 10:1757-1771 (2000).  
 RL [8]

RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kuribara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/NCBI databases.  
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 CC  
 EMBL; AK028112; BAC25753.1; -; mRNA.  
 DR HSSP; P08631; 1AD5.  
 DR SMR; Q8CE10; 46-491.  
 DR Ensembl; ENSMUSG00000042228; Mus musculus.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IDA.  
 DR GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.

DR GO; GO:0046777; P:protein amino acid autophosphorylation; IDA.  
 DR GO; GO:0046777; P:protein amino acid autophosphorylation; TAS.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser-thr\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam; PF007714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00401; SH3; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD00001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000065; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyrKC; 1.

Query Match Score 86.3%; DB 2; Length 491;  
 Best Local Similarity 80.0%; Pred. No. 22;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Db 470 DYLOQSVLDF 479

RESULT 17  
 Q5ZMB9 CHICK  
 ID Q5ZMB9-CHICK PRELIMINARY; PRT; 492 AA.  
 AC Q5ZMB9;  
 DT 23-NOV-2004, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 8.  
 DE Hypothetical protein.  
 ORFNames=RCJMB04\_2j8;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 NCBI\_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CB; TISSUE=Bursa;  
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,  
 RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Kotter M.,  
 RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;  
 RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate  
 RT genefunction analysis.";  
 RT Genome Biol. 6:R6-R6 (2005).  
 RL CC  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC  
 EMBL; AJ719465; CAG31124.1; -; mRNA.  
 DR SMR; Q5ZMB9; 46-492.  
 DR GO; GO:0005524; F:PTB binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser-thr\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR01452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR InterPro; IPR008266; Tyr\_pkinase\_AS.  
 DR Pfam; PF007714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR PRINTS; PR00401; SH3DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE..  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 SMART; SM00219; TYRK; 1.  
 PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 PROSITE; PS50001; SH2; 1.  
 PROSITE; PS50002; SH3; 1.  
 KW Hypothetical protein.  
 SEQUENCE 492 AA; 56202 MW; 69D2F0534E33CC1E CRC64;

Query Match 86.3%; Score 44; DB 2; Length 492;  
 Best Local Similarity 80.0%; Pred. No. 22; Mismatches 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QV 1 DYLRSVLEDF 10  
 ||||:||||:|||  
 Db 471 DYLQSVLDDF 480

RESULT 18

ID	LYN_HUMAN	STANDARD;	PRT;	511 AA.
AC	P07948;			
DT	01-AUG-1988, integrated into UniProtKB/Swiss-Prot.			
DT	01-JUN-1994, sequence version 2.			
DT	07-MAR-2006, entry version 74.			
DE	Tyrosine-protein kinase Lyn (EC 2.7.1.112).			
GN	Name=LYN;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [mRNA].			
RX	MEDLINE=87172710; PubMed=3561390;			
RA	Yamanashi Y., Fukushima S., Semba K., Sukegawa J., Miyajima N.,			
RA	Matsubara K., Yamamoto T., Toyoshima K.;			
RT	"The yes-related cellular gene lyn encodes a possible tyrosine kinase similar to p56lck."			
RT	Mol. Cell. Biol. 7:237-243 (1987).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [mRNA].			
RX	MEDLINE=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;			
RA	Rider L.G., Raben N., Miller L., Jelsema C.;			
RT	"The cDNAs encoding two forms of the LYN protein tyrosine kinase are expressed in rat mast cells and human myeloid cells.";			
RL	Gene 138:219-222 (1994).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM LYN A).			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klaunser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			

RA RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RT RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE [mRNA] OF 368-423.  
 MEDLINE=91062389; PubMed=2247464;  
 RA Partanen J., Maekela T.P., Alitalo R., Lehtaevaaho H., Alitalo K.;  
 RT "Putative tyrosine kinases expressed in K-562 human leukemia cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917 (1990).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [mRNA] OF 368-423.  
 MEDLINE=92378604; PubMed=1510669;  
 RA Bielke W., Ziemienski A., Kappos L., Miescher G.C.;  
 RT "Expression of the B cell-associated tyrosine kinase gene Lyn in primary neuroblastoma tumours and its modulation during the differentiation of neuroblastoma cell lines.";  
 RT RL Biochem. Biophys. Res. Commun. 186:1403-1409 (1992).  
 RN [6]  
 RP INTERACTION WITH EPSTEIN-BARR VIRUS LMP2A.  
 RX Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,  
 RA Zha X.-M., Polakiewicz R.D., Comb M.J.;  
 RA Bolen J.B., Kieff E.;  
 RT "Integral membrane protein 2 of Epstein-Barr virus regulates reactivation from latency through dominant negative effects on protein-tyrosine kinases.";  
 RT RL Immunity 2:155-166 (1995).  
 RN [7]  
 RP PHOSPHORYLATION SITE TYR-507, AND MASS SPECTROMETRY.  
 RX PubMed=15592455; DOI=10.1038/nbt1046;  
 RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,  
 RA Zha X.-M., Polakiewicz R.D., Comb M.J.;  
 RT "Immunoaffinity profiling of tyrosine phosphorylation in cancer cells.";  
 RT RL Biotechnol. 23:94-101 (2005).  
 CC "-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine phosphate.  
 CC "-!- SUBUNIT: Interacts with phosphorylated LIM1 upon BCR activation.  
 CC "-!- INTERACTION:  
 CC O92969:- (xeno); NbExp=2; IntAct=EBI-79452, EBI-710506;  
 CC P26660:- (xeno); NbExp=1; IntAct=EBI-79452, EBI-706322;  
 CC P27958:- (xeno); NbExp=5; IntAct=EBI-79452, EBI-706378;  
 CC Q9WMX2:- (xeno); NbExp=2; IntAct=EBI-79452, EBI-710918;  
 CC P20273:CD22; NbExp=1; IntAct=EBI-79452, EBI-78277;  
 CC Q6NVF1:Centd3 (xeno); NbExp=2; IntAct=EBI-79452, EBI-621463;  
 CC P67870:CSNK2B; NbExp=1; IntAct=EBI-79452, EBI-348169;  
 CC Q9UIF2:gPVI; NbExp=2; IntAct=EBI-79452, EBI-515278;  
 CC Q07666:KHDRBS1; NbExp=1; IntAct=EBI-79452, EBI-1364;  
 CC "-!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=LYN A;  
 CC IsoID=P07948-1; Sequence=Displayed;  
 CC Name=LYN B;  
 CC IsoID=P07948-2; Sequence=vSP\_005002;  
 CC "-!- TISSUE SPECIFICITY: Expressed in primary neuroblastoma tumors.  
 CC "-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC subfamily.  
 CC "-!- SIMILARITY: Contains 1 SH2 domain.  
 CC "-!- SIMILARITY: Contains 1 SH3 domain.  
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 CC EMBL; M16038; AAA59540.1; -; mRNA.  
 DR EMBL; M79321; AAB50019.1; -; mRNA.  
 DR EMBL; BC075001; AAH75001.1; -; mRNA.  
 DR EMBL; BC075002; AAH75002.1; -; mRNA.  
 DR PIR; A26719; TVHUY.  
 DR PDB; 1WLF; NMR; A=60-122.  
 DR PDB; 1WA7; NMR; A=60-122.  
 DR SMR; P07948; 66-511.  
 DR IntAct; P07948; -.

DR Ensembl; ENSG00000147507; Homo sapiens.  
 DR HGNC; HGNC:6735; LYN.  
 DR MIM; 165120; gene.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . . ; TAS.  
 DR GO; GO:0006458; P:protein amino acid phosphorylation; TAS.  
 DR GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR000719; prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PRO00401; SH2DOMAIN.  
 DR PRINTS; PRO00452; SH3DOMAIN.  
 DR PRINTS; PRO00109; TYRKINASE.  
 DR PRODom; PD000001; Prot\_kinase; 1.  
 DR PRODom; PD000093; SH2; 1.  
 DR PRODom; PD000066; SH3; 1.  
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 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS00001; SH2; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW 3D-structure; Alternative splicing; ATP-binding; Kinase; Lipoprotein;  
 KW Myristate; Nucleotide-binding; Phosphorylation;  
 KW Proto-oncogene; SH2\_domain; SH3\_domain; Transferase;  
 KW Tyrosine-protein kinase.  
 FT INIT MET 0 0  
 FT CHAIN 1 511  
 BY similarity.  
 TYROSINE-PROTEIN KINASE LYN.  
 /FTId=PRO\_0000088129.

FT DOMAIN 62 122  
 FT DOMAIN 128 225  
 FT DOMAIN 246 500  
 FT NP\_BIND 252 260  
 FT ACT\_SITE 366 366  
 FT BINDING 274 274  
 FT MOD\_RES 396 396  
 MOD RES 507 507  
 FT LIPID 1 1  
 FT LIPID 2 2  
 FT VARSPLIC 22 42  
 FT STRAND 65 71  
 FT STRAND 73 73  
 FT STRAND 77 79  
 FT STRAND 83 83  
 FT TURN 85 86  
 FT STRAND 88 94  
 FT STRAND 96 103  
 FT TURN 104 106  
 FT STRAND 109 113  
 FT TURN 114 116  
 FT STRAND 117 119  
 SQ SEQUENCE 511 AA; 58443 MW; 8419CD461204E364 CRC64;

Query Match Best Local Similarity 86.3%; Score 44; DB 1; Length 511;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DYIIRSVLED 10  
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 Db 490 DYLOQSVLDDF 499

DR LYN\_MOUSE ID LYN\_MOUSE STANDARD; PRT; 511 AA.  
 DR AC P25911; Q62127;  
 DT 01-MAY-1992; integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1997; sequence version 3.  
 DT 07-MAR-2006; entry version 64.  
 DE Tyrosine-protein kinase Lyn (EC 2.7.1.112).  
 GN Name=Lyn;  
 OS Mus musculus (Mouse).  
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 CC Muroidea; Muridae; Murinae; Mus.  
 CC NCBI\_TAXID=10090;  
 RN [1]  
 RP NUCLEOTIDE\_SEQUENCE [mRNA].  
 RX MEDLINE=91260688; PubMed=1710766;  
 RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A., Lock P.,  
 RA Dunn A.R.;  
 RT "Alternatively spliced murine lyn mRNAs encode distinct proteins.";  
 RL Mol. Cell. Biol. 11:3399-3406(1991).  
 RN [2]  
 RP NUCLEOTIDE\_SEQUENCE [mRNA].  
 RX MEDLINE=91203857; PubMed=2017160;  
 RA Yi T., Bolen J.B., Ihle J.N.;  
 RT "Hematopoietic cells express two forms of lyn kinase differing by 21  
 amino acids in the amino terminus.";  
 RL Mol. Cell. Biol. 11:2391-2398(1991).  
 RN [3]  
 RP NUCLEOTIDE\_SEQUENCE [LARGE\_SCALE mRNA] (ISOFORM LYN A).  
 RC STRAIN=Czech II; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marras M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RL [4]  
 RN NUCLEOTIDE\_SEQUENCE [mRNA] OF 363-431.  
 RX MEDLINE=90152381; PubMed=2482828; DOI=10.1016/0378-1119(89)90465-4;  
 RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;  
 RT "The application of the polymerase chain reaction to cloning members  
 RT of the protein tyrosine kinase family.";  
 RL Gene 85:67-74 (1989).  
 RN [5]  
 RP INTERACTION\_WITH\_LIME1.  
 RX PubMed=16249387; DOI=10.1182/blood-2005-05-1859;  
 RA Ahn E., Lee H., Yun Y.;  
 RT "LIME acts as a transmembrane adapter mediating BCR-dependent B-cell  
 activation.";  
 RL Blood 107:1521-1527(2006).  
 CC -- CATALYTIC\_ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 CC tyrosine phosphate.  
 CC -- SUBUNIT: Interacts with phosphorylated LIME1 upon BCR activation.  
 CC -- ALTERNATIVE\_PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC IsoID=P25911-1; Sequence=Displayed;  
 CC Name=LYN A;  
 CC Name=LYN B;

CC	-!- TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and myeloid cells.	FT	CONFLICT	414	414	I -> F (in Ref. 4).
CC	-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC subfamily.	FT	CONFLICT	424	424	D -> N (in Ref. 1).
CC	-!- SIMILARITY: Contains 1 SH2 domain.	FT	SEQUENCE	431	431	L -> P (in Ref. 4).
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>	FT	SEQUENCE	511 AA;	58681 MW;	3935221CC90C50FO CRC64;
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CC	P -> L (in Ref. 2).	DB	490 DYLQSVLDDF 499	:    :		
CC	V -> I (in Ref. 2).					
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DR	EMBL; M33426; AAA40017.1; -; mRNA.	PRT				
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DR	SMR; P25911; 66-511.	DT	01-JUN-1994, integrated into UniProtKB/Swiss-Prot.			
DR	IntAct; P25911; -.	DT	01-NOV-1997, sequence version 2.			
DR	Ensembl; ENSMUSG0000042228; Mus musculus.	DT	07-MAR-2006, entry version 57.			
DR	MGI; MGI; 96892; Lyn.	DE	Tyrosine-protein kinase Lyn (EC 2.7.1.112).			
DR	GO; GO:0005515; F:protein binding; IPI.	GN	Name=Lyn;			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.	OS	Rattus norvegicus (Rat).			
DR	GO; GO:0046777; P:autophosphorylation; IDA.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DR	GO; GO:0007242; P:intracellular signaling cascade; IDA.	OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
DR	GO; GO:0018108; P:peptidyl-tyrosine phosphorylation; IDA.	OC	Muroidea; Muridae; Murinae; Rattus.			
DR	InterPro; IPR000719; Prot kinase.	OX	NCBI_TaxID=10116;			
DR	InterPro; IPR002290; Ser_thr_Pkinase.	RN	[1]			
DR	InterPro; IPR000980; SH2.	RP	NUCLEOTIDE SEQUENCE [mRNA].			
DR	InterPro; IPR001452; SH3.	RA	Minoguchi K., Nishikata H., Siraganian R.P.;			
DR	InterPro; IPR001245; Tyr_Pkinase.	RT	"Bacterially expressed rat p56lyn binds several proteins in rat			
DR	InterPro; IPR008266; Tyr_Pkinase_AS.	RT	basophilic leukemia cells including pp72, a tyrosine phosphorylated			
DR	pfam; PF00714; Pkinase_Tyr; 1.	RT	protein prominent in activated cells.";			
DR	pfam; PF00017; SH2; 1.	RL	J. Immunol. 150:222-222(1993).			
DR	PRINTS; PR00401; SH2DOMAIN.	RN	[2]			
DR	PRINTS; PR00109; TYRKINASE.	RP	NUCLEOTIDE SEQUENCE [mRNA].			
DR	ProDom; PD000001; Prot_kinase; 1.	RX	Medline=94171041; PubMed=8125304; DOI=10.1016/0378-1119(94)90811-7;			
DR	ProDom; PD000093; SH2; 1.	RA	Rider L.G., Miller L., Jelissema C.;			
DR	ProDom; PD000066; SH3; 1.	RT	"The cDNAs encoding two forms of the LYN Protein tyrosine kinase are			
DR	SMART; SM00252; SH2; 1.	RT	expressed in rat mast cells and human myeloid cells.";			
DR	SMART; SM00326; SH3; 1.	RL	Gene 138:219-222(1994).			
DR	SMART; SM00219; TYRKc; 1.	RN	[3]			
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DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.	RA	Vonakoch B.M., Chen H., Haleem-Smith H., Metzger H.;			
DR	PROSITE; PS50001; SH2; 1.	RT	"The unique domain as the site on Lyn kinase for its constitutive			
DR	PROSITE; PS50002; SH3; 1.	RT	association with the high affinity receptor for IgE.";			
KW	Alternative splicing; ATP-binding; Kinase; Lipoprotein; Myristate; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase.	RL	J. Biol. Chem. 272:24072-24080(1997).			
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FT	DOMAIN 246 500 ATP (By similarity).	CC	Name=LYN A;			
FT	NP_BIND 252 260 Proton acceptor (By similarity).	CC	Name=LYN B;			
FT	ACT_SITE 366 366 ATP (By similarity).	CC	IsoId=Q07014-2; Sequence=VSP_005004;			
FT	BINDING 274 274 Phosphotyrosine (by autocatalysis) (By similarity).	CC	-!- TISSUE SPECIFICITY: Expressed predominantly in B-lymphoid and			
FT	MOD_RES 396 396 Phosphotyrosine (By similarity).	CC	myeloid cells.			
FT	MOD_RES 507 507 N-myristoyl glycine (By similarity).	CC	-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC			
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FT	CONFLICT 76 76 (in Ref. 2).	CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>			
FT	CONFLICT 160 160 (in Ref. 2).	CC	Distributed under the Creative Commons Attribution-NoDerivs License			
FT	CONFLICT 278 278 (in Ref. 2).	CC	/FTId=VSP_005003.			
FT	CONFLICT 390 390 (in Ref. 2).	CC	DR			
FT	CONFLICT 76 76 (in Ref. 2).	EMBL; L14782; AAA20944.1; -; mRNA.				
FT	CONFICT 160 160 (in Ref. 2).	EMBL; L14823; AAA20945.1; -; mRNA.				
FT	CONFLICT 278 278 (in Ref. 2).	EMBL; AF000300; AAB71344.1; -; mRNA.				
FT	CONFLICT 390 390 (in Ref. 2).	EMBL; AF000301; AAB71345.1; -; mRNA.				

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 DR PIR; I56160; I56160.  
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 DR RGD; 621017; Lyn.  
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 DR InterPro; IPR001452; SH3.  
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 DR Pfam; PF00018; SH3; 1; 1.  
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 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
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 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TyrKC; 1.  
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 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
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 DR PROSITE; PS50002; SH3; 1.  
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 FT DOMAIN 62 122  
 FT DOMAIN 128 225  
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 FT NP\_BIND 252 260  
 FT ACT\_SITE 366 366  
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 FT VARSPLIC 24 44  
 FT MOD\_RES 507 507  
 FT CONFLICT 307 307  
 FT CONFLICT 418 418  
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 Best Local Similarity 80.0%; Pred. No. 23;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYLRSVLEDF 10  
 Db 490 DYLOSVLDDF 499

RESULT 21  
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 AC Q3TC53;  
 DT 11-OCT-2005, integrated into UniProtKB/TREMBL.  
 DT 11-OCT-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE NOP-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:R630107015 product:Yamaguchi sarcoma viral (v-yes-1) oncogene homolog, full insert sequence (Bone marrow macrophage cDNA,

DE RIKEN full-length enriched library, clone:I830054M12 product:Yamaguchi sarcoma viral (v-yes-1) oncogene homolog, full insert sequence).  
 DE OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";  
 RT Methods Enzymol. 303:19-44(1999).  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Kattayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bjelic V.B., Brenner S.E., Batyalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aiddins V., Allen J.E., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgini-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollrias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuza S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Semo S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmold S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., RA Iida J., Immura K., Itoh M., Kato T., Kawaji H., Kawagashira N., RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., RA Hayashizaki Y.; "The transcriptional landscape of the mammalian genome.";  
 RN Science 309:1559-1563 (2005).  
 [3]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566 (2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=NOD, and C57BL/6J; TISSUE=Bone marrow;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osoyo N., Saito R., Suzuki H., Yamamoto T., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,







LCK CHICK STANDARD; PRT; 507 AA.

ID P42683; Q53WS8; AC 01-NOV-1995, integrated into UniProtKB/Swiss-Prot. DT 01-NOV-1995, sequence version 1. DT 07-MAR-2006, entry version 47.

DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-tyrosine kinase C-TKL) (p56tk1). GN Name=LCK; OS Gallus gallus (Chicken). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. OC NCBI\_TaxID=9031; [1]

RP NUCLEOTIDE SEQUENCE [mRNA]. TISSUE=Spleen; RC Gaertner T., Khnel H., Strebhardt K., Ruebsamen-Waigmann H.; RA Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases. RL [2]

RP NUCLEOTIDE SEQUENCE [mRNA] OF 1-88. RX MEDLINE=92186854; PubMed=1545804; RA Chow L., Ratcliffe M., Veillette A.; RT "t<sub>k</sub>l is the avian homolog of the mammalian lck tyrosine protein kinase gene."; RL Mol. Cell. Biol. 12:1226-1233 (1992). RN [3]

RP NUCLEOTIDE SEQUENCE [mRNA] OF 46-507. RX MEDLINE=88097370; PubMed=3321053; RA Strebhardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.; RT Additional member of the protein-tyrosine kinase family: the src- and lck-related protooncogene c-tkl.; Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).

CC -!- FUNCTION: Tyrosine kinase that plays an essential role for the selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor(TCR)-linked signal transduction pathways (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein CC -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD4, CD8 (By similarity).

CC -!- SUBCELLULAR LOCATION: Bound to the cytoplasmic domain of either CC CD4 or CD8 (By similarity). CC -!- PTM: Phosphorylated on Tyr-503. This phosphorylation downregulates catalytic activity. Phosphorylated on Tyr-392 either by itself or another kinase, leading to increased enzymatic activity. CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC CC -!- SIMILARITY: Contains 1 SH2 domain. CC -!- SIMILARITY: Contains 1 SH3 domain.

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DR EMBL: X60380; CAA42930.1; -; mRNA. DR EMBL: M85043; AAA49003.1; -; mRNA. DR EMBL: J03579; AAA49081.1; ALT\_INIT; mRNA. DR HSSP; P06239; 3LCK. DR InterPro; IPR000719; Prot\_kinase. DR InterPro; IPR002290; Ser\_Thr\_pkinase. DR InterPro; IPR000980; SH2. DR InterPro; IPR001452; SH3. DR InterPro; IPR001245; Tyr\_pkinase. DR InterPro; IPR00266; Tyr\_pkinase\_AS. DR Pfam; PF00017; SH2; 1. DR Pfam; PF00018; SH3\_1; 1. DR PRINTS; PR00401; SH2DOMAIN. DR PRINTS; PR00452; SH3DOMAIN. DR PRINTS; PR00109; TYRKINASE. DR ProdDom; PD000001; Prot\_kinase; 1.

DR ProDom; PD000093; SH2; 1. DR ProDom; PD000066; SH3; 1. DR SMART; SM00252; SH2; 1. DR SMART; SM00326; SH3; 1. DR SMART; SM00219; TYRK; 1. DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1. DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1. DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1. DR PROSITE; PS50001; SH2; 1. DR PROSITE; PS50002; SH3; 1. DR ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase. KW ATP-binding; Kinase; Lipoprotein; Membrane; Myristate; Nucleotide-binding; Palmitate; Phosphorylation; Proto-oncogene; SH2 domain; SH3 domain; Transferase; Tyrosine-protein kinase. KW INIT\_MER 0 0 Probable.

FT CHAIN 1 507 Proto-oncogene tyrosine-protein kinase LCK. FT /FTId=PRO\_0000088128.

FT DOMAIN 59 119 SH3.

FT DOMAIN 125 222 SH2.

FT DOMAIN 243 496 Protein kinase.

FT NP\_BIND 249 496 ATP (By similarity).

FT ACT\_SITE 362 362 Proton acceptor (By similarity).

FT BINDING 271 271 ATP (By similarity).

FT MOD\_RES 392 392 Phosphotyrosine (by autocatalysis) (By similarity).

FT MOD\_RES 503 503 Phosphotyrosine (negative regulation) (By similarity).

FT LIPID 1 1 N-myristoyl glycine (By similarity).

FT LIPID 2 2 S-palmitoyl cysteine (By similarity).

FT LIPID 4 4 S-palmitoyl cysteine (By similarity).

FT SEQUENCE 507 AA; 58009 MW; BC83C4FA891B5170 CRC64;

Query Match Best Local Similarity 70.0%; Pred. No. 54; Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0; Qy 1 DYLRSVLEDF 10 Db 486 EYMKSVLED 495

RESULT 27

Q66104 BRARE ID Q66104\_BRARE PRELIMINARY; PRT; 510 AA.

AC Q66104- BRARE

DT 11-OCT-2004, integrated into UniProtKB/TREMBL. DT 07-FEB-2006, entry version 11.

DE Zgc: 92124.

GN ORFNames=zgc:92124; OS Brachydanio rerio (Zebrafish) (Danio rerio)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio. OC NCBI\_TaxID=7955; [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole; RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Ronald M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,  
 RA Schnerr A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Whole;  
 RA Director MGC Project;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.  
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 CC  
 EMBL; BC081601; AAH81601.1; -; mRNA.  
 SMR; Q66I04; 65-510.  
 Ensembl; ENSDARG0000031715; Danio rerio.  
 ZFIN; ZDB-GENE-040912-7; zgc:92124.  
 GO; GO:0005524; F:ATP binding; IEA.  
 GO; GO:0004713; F:protein-tirosine kinase activity; IEA.  
 GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00719; Prot kinase.  
 DR InterPro; IPR002290; Ser-thr\_pk kinase.  
 DR InterPro; IPR00980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 PRINTS; PR00452; SH3DOMAIN.  
 PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000093; Prot\_kinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK\_C; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR SEQUENCE; 510 AA; 58258 MW; 5EE8F68226569BA2 CRC64;  
 DR  
 QY 1 DYLRSLVLED 10  
 Db 489 DYIQSVLDDF 498  
 RESULT 28  
 Q5RHX5\_BRARE PRELIMINARY; PRT; 196 AA.  
 ID Q5RHX5\_BRARE PRELIMINARY; PRT; 196 AA.  
 AC Q5RHX5;  
 DT 21-DEC-2004, integrated into UniProtKB/TREMBL.  
 DT 21-DEC-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 7.  
 DE Novel protein.  
 GN Name=si:ch211-1494.1; Synonyms=ORTDARP00000006609;  
 GN ORFNames=CH211-14G4.1-002;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 RN NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Gray E.;  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.  
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 CC  
 EMBL; BX323889; CAII1616.1; ALT INIT; Genomic\_DNA.  
 ZFIN; ZDB-GENE-041014-248; si:ch211-1494.1.  
 InterPro; IPR005176; DUF298.  
 DR Pfam; PF03556; DUF298; 1.  
 FT CHAIN; 1 280 DCNL1-like protein 4.  
 FT DOMAIN 161 275 DCNL1.  
 FT /FTId=PRO\_0000129505.  
 SQ SEQUENCE 280 AA; 32421 MW; A0C354AAC15688C CRC64;  
 DR  
 QY 1 DYLRSLVLED 9  
 Db 169 DYIQSVLND 177  
 RESULT 30  
 Q4RKU7\_TETNG PRELIMINARY; PRT; 281 AA.  
 ID Q4RKU7\_TETNG PRELIMINARY; PRT; 281 AA.  
 AC Q4RKU7;  
 DT 19-JUL-2005, integrated into UniProtKB/TREMBL.  
 RN [1]

DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 DE Chromosome 1 SCAF15025, whole genome shotgun sequence. (Fragment).  
 GN ORFNames=GSTENG0032781001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetradontoidea; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15496914; DOI=10.1038/nature03025;  
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Gaffé D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Biémont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,  
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype.";  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
 CC ! - CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC  
 DR EMBL; CAAE0115025; CAGI0985.1; -; Genomic\_DNA.  
 DR InterPro; IPR005176; DUF298.  
 DR PANTHER; PTHR12281; DUF298; 1.  
 DR Pfam; PF03556; DUF298; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 281 281  
 SQ SEQUENCE 281 AA; 32851 MW; 35EDC7C4ED12D8C9 CRC64;

Query Match 78.4%; Score 40; DB 2; Length 281;

Best Local Similarity 88.9%; Pred. No. 69; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0;

Qy	1 DYLRSVLED	9
Db	170 DYLRSLND	178

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GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on:

June 29, 2006, 08:59:14 ; Search time 87.8313 Seconds

(without alignments)

46.851 Million cell updates/sec

Title: US-10-062-257A-3  
 Perfect score: 50  
 Sequence: 1 HYTNASDGL 9

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004as:\*

9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description
1	50	100.0	9	4	AAB73119	Abt73119 Tumour an-
2	50	100.0	9	6	ABR84375	Abr84375 Human lck
3	50	100.0	9	8	ADS87116	Ads87116 Human gen
4	50	100.0	9	9	ADX58315	Adx58315 Partial a
5	50	100.0	9	9	ADZ42230	Adz42230 Cytotoxic
6	50	100.0	9	9	AEC33131	Aec33131 Lck tumor
7	50	100.0	9	10	AAE99213	Aee99213 Cancer an-
8	50	100.0	98	7	ADN11799	Adn11799 lck SH2 d
9	50	100.0	101	2	AAW31184	AAw31184 Human p56
10	50	100.0	102	2	AAR60992	Aar60992 Fragment
11	50	100.0	102	2	AAR72090	Aar72090 lck SH2 r
12	50	100.0	134	2	AAW03982	AAw03982 DET1-DET2
13	50	100.0	134	2	AAW02120	AAw02120 DET1-DET2
14	50	100.0	134	2	AAW11286	AAw11286 DET1-DET2
15	50	100.0	134	2	AAW19624	AAw19624 Human lck
16	50	100.0	224	2	AAW14788	AAw14788 FKB-P-LCK:
17	50	100.0	224	2	AAW96823	AAw96823 A fusion
18	50	100.0	363	6	ABR59690	Abt59690 Human p56
19	50	100.0	363	8	ADP48375	Adp48375 Human lym
20	50	100.0	437	5	ABG79672	Abg79672 Tumour in
21	50	100.0	508	3	AB37700	Ab37700 Human lym
22	50	100.0	508	7	ADE58802	Ad58802 Human Pro
23	50	100.0	508	7	ADE58799	Ad58799 Human Pro

24	50	100.0	508	7	ADF45072	Adf45072 Human kin
25	50	100.0	508	7	ADL34479	Adl34479 Human lym
26	50	100.0	508	8	ADS88148	Ad88148 Human pro
27	50	100.0	509	3	AAY49420	Aay49420 PKA subst
28	50	100.0	509	6	ABR58699	Abr58699 Human can
29	50	100.0	509	7	ABR56202	Abr56202 Human lym
30	50	100.0	509	7	ADE40449	Ade40449 Human pro
31	50	100.0	509	8	ADL22907	Adl22907 Human Mp2
32	50	100.0	509	8	ADP12458	Adp12458 Protein e
33	50	100.0	509	8	ADP48374	Adp48374 Human lym
34	50	100.0	509	9	ADZ51107	Adz51107 Amino aci
35	50	100.0	509	9	AEA35921	Aea35921 Human Lck
36	50	100.0	509	8	ABM82981	Abm82981 Human dia
37	50	100.0	539	8	ABM82982	Abm82982 Human dia
38	50	100.0	539	2	ABG79673	Abg79673 Tumour in
39	40	80.0	193	2	AAR63367	Aar63367 Peptide f
40	40	80.0	298	2	AAR84183	Aar84183 Megakaryo
41	40	80.0	505	6	ABU08941	Abu08941 Human nuc
42	40	80.0	505	6	ADN25600	Adn25600 Bacterial
43	40	80.0	505	2	AAR85929	Aar85929 Protein t
44	40	80.0	505	6	ABU70942	Abu70942 Human adi
45	40	80.0	505	6	ABU08943	Abu08943 Human nuc
46	40	80.0	505	6	ABU8944	Abu8944 Human nuc
47	40	80.0	382	8	ADS27093	Ad527093 Bacterial
48	40	80.0	382	8	AAD26341	Ad526341 Bacterial
49	49	74.0	37	74.0	ADN25600	Adn25600 Bacterial
50	50	74.0	37	74.0	AEA15030	Aea15030 pTRG Lox
51	51	74.0	36	72.0	ABG95124	Abg95124 Human c-s
52	52	74.0	36	72.0	ADR39735	Adr39735 Human kin
53	53	74.0	36	72.0	AAR52824	Adr52824 GTP-cyclo
54	54	74.0	36	72.0	AAU78677	Aau78677 Human SH2
55	55	74.0	36	72.0	AAY49418	Aay49418 PKA subst
56	56	74.0	36	72.0	AAY44448	Aay44448 Wild-type
57	57	74.0	36	72.0	AAG67623	Aag67623 Amino aci
58	58	74.0	36	72.0	AAB84662	Aab84662 Amino aci
59	59	74.0	36	72.0	AAG67444	Aag67444 Amino aci
60	60	74.0	36	72.0	ABR47428	Abt47428 Breast ca
61	61	74.0	36	72.0	ABR59696	Abt59696 Human c-s
62	62	74.0	36	72.0	ABO07208	Abt07208 Human p53
63	63	74.0	36	72.0	AAD63739	Ada63739 Human pro
64	64	74.0	36	72.0	ADF45046	Adf45046 Human kin
65	65	74.0	36	72.0	ADP48375	Adp48375 Human c-s
66	66	74.0	36	72.0	ADP48375	Adp48375 Human c-s
67	67	74.0	36	72.0	ADP48375	Adp48375 Human c-s
68	68	74.0	36	72.0	ADP48375	Adp48375 Human c-s
69	69	74.0	36	72.0	ADP48375	Adp48375 Human c-s
70	70	74.0	459	4	AAO13873	Aao13873 Human pol
71	71	74.0	459	9	AEA20969	Aea20969 Novel hum
72	72	74.0	459	9	ADL57015	Adl57015 Csk. 5/20
73	73	74.0	463	7	AEA20073	Aea20073 Novel hum
74	74	74.0	463	9	Aea07015	Aea07015 Csk. 5/20
75	75	74.0	463	9	Abr84178	Abt84178 Human dia
76	76	74.0	485	8	Abm84181	Abm84181 Human dia
77	77	74.0	485	8	Abm84179	Abm84179 Human dia
78	78	74.0	505	4	Abb71008	Abb71008 Drosophil
79	79	74.0	511	8	ABM84182	Abt84182 Human dia
80	80	74.0	511	8	ABM84180	Abt84180 Human dia
81	81	97	7	ADN11796	Adn11796 C-YEES SH2	
82	82	104	2	AAW06343	Aaw06343 Streptomy	
83	83	179	4	ABG30013	Abg30013 Novel hum	
84	84	197	6	ABP68430	Abp68430 Human col	
85	85	230	4	ABG30014	Abg30014 Novel hum	
86	86	263	2	AAW02120	Aaw02120 DET1-DET2	
87	87	303	4	ABG26073	Abg26073 Novel hum	

				OS	Homo sapiens.
97	35	70.0	451	7	ADD46393 Rat prote
98	35	70.0	498	7	Adf05197 Bacterial
99	35	70.0	499	8	Abm84206 Human dia
100	35	70.0	543	2	Aay24421 Human Yes
ALIGNMENTS					
RESULT 1					
AAB73119	ID	AAB73119 standard; peptide; 9 AA.			
XX	AC	AAB73119;			
XX	DT	09-MAY-2001 (first entry)			
XX	DE	Tumour antigen peptide #3.			
XX	KW	Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.			
XX	OS	Homo sapiens.			
XX	PN	WO200111044-A1.			
XX	PD	18-DEC-2002.			
XX	PF	18-SEP-2001; 2001JP-00283413.			
XX	PR	13-NOV-2000; 2000JP-00345094.			
XX	PA	(ITOV/) ITO Y.			
XX	DR	WPI; 2003-508315/48.			
PS	Example 8; Page 10; 18pp; Japanese.				
XX	CC	The invention relates to a method for the detection of antigen specific T			
CC	CC	-cells in a blood sample involving the use of a plurality of antigenic			
CC	CC	peptides. The method comprises sampling of peripheral blood monocytes;			
CC	CC	stimulation of the collected peripheral blood monocytes with antigens			
CC	CC	without direct use of antigen presenting cells; and detection of T-cells			
CC	CC	specific to the antigen in the stimulated monocytes. The method is			
CC	CC	particularly used for the detection of cancer as it can be used in semi-			
CC	CC	quantitative determination of cancer specific T-cells. It can also be			
CC	CC	used for cancer vaccine therapy for patients with cervical or prostate			
CC	CC	cancer. The method can additionally be used to monitor of cellular			
CC	CC	immunity and cancer immune therapy by detection of specific T-cell			
CC	CC	frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human			
CC	CC	leukocyte antigen) peptides of human origin used in an example from the			
PI	CC	invention			
XX	DR	Itoh K;			
XX	PT	WPI; 2001-191541/19.			
XX	PT	Tumor antigen peptides which induce tumor-specific cytotoxic T-cells and			
XX	PT	polynucleotides encoding them for treatment of cancer.			
PS	Claim 1; Page 66; 75pp; Japanese.				
XX	CC	The present invention relates to peptides which are partial sequences of			
CC	CC	src/lck family proteins. The present sequence is one such peptide. The			
CC	CC	peptides are useful for producing vaccines for the treatment of cancer,			
CC	CC	including colon cancer and small-cell lung cancer			
XX	SQ	Sequence 9 AA;			
XX	Query Match	100.0%; Score 50; DB 4; Length 9;			
XX	Best Local Similarity	100.0%; Pred. No. 2.1e+06;			
Matches	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 HYTNASDGL 9				
Db	1 HYTNASDGL 9				
RESULT 3					
ADS87116	ID	ADS87116 standard; peptide; 9 AA.			
XX	AC	ADS87116;			
XX	DT	18-NOV-2004 (First entry)			
XX	DE	Human genetic vaccine/ubiquitin (Ub)/Lck-related epitope peptide 1.			
XX	KW	vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;			
XX	KW	Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;			
XX	KW	lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;			
XX	KW	colon; bladder; breast; oesophagus; kidney; brain; human; epitope; Lck.			
OS	OS	Homo sapiens.			
XX	XX	WO2004035085-A1.			
XX	PD	29-APR-2004.			
XX	PF	16-OCT-2003; 2003WO-JP013279.			
XX	PR	17-OCT-2002; 2002JP-00302816.			
XX	PR	(KYUS-) KYUSHU TLO CO LTD.			
XX	XX				
DE	Human lck HLA-A24 epitope, SEQ ID NO:25.				
XX	Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;				
KW	KW	cancer; tumour; cervical cancer; prostate cancer; cellular immunity;			
KW	KW	immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;			
KW	KW	human; human leukocyte antigen; HLA-A24 epitope.			

PI Himeno K, Furue M, Maehara Y;  
 XX DR WPI; 2004-357144/33.

PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes  
 PT or cytokine genes for prevention and treatment of cancer.

XX Disclosure; SEQ ID NO 132; 266pp; Japanese.

CC The invention relates to a novel genetic vaccine containing the ubiquitin gene together with a gene encoding an antigenic protein containing a T-cell target sequence. The vaccine of the invention may be useful for prevention and treatment of cancers including melanoma, sarcoma, lymphoma (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas, colon, bladder, breast, oesophagus, kidney or brain. The current sequence is that of a human genetic vaccine/ubiquitin (Ub)-related epitope peptide of the invention.

CC Sequence 9 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 5

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0	Mismatches	0
		Indels	0
		Gaps	0

QY 1 HYTNASDGL 9  
 Db 1 HYTNASDGL 9

Db Sequence 9 AA;

RESULT 4

Query Match	Score	DB	Length
Best Local Similarity	100.0%	9	9
Matches	9	0	0
Conservative	0		

RESULT 6		DT 23-FEB-2006 (first entry)
ID AEC33131	DE XX	Cancer antigen lck peptide SEQ ID NO 3.
ID AEC33131 standard; peptide; 9 AA.	ID XX	
AC AEC33131;	KW XX	Cytostatic; Vaccine; cancer; neoplasm; antigen; lck.
XX	OS XX	Unidentified.
DE XX	PR XX	21-JUN-2004; 2004JP-00182811.
DT XX	PA XX	(UYKU-) UNIV KURUME.
XX	PI XX	Itoh K;
PD XX	DR XX	WPI; 2006-057212/06.
PF XX	PT XX	Treating cancer by evaluating specific cytotoxic T-lymphocyte precursors for each peptide of cancer antigen peptide set, in patient, administering peptide set obtained after removing peptide being non-specific to precursors, to patient.
PR XX	PT XX	Example 1; SEQ ID NO 3; 36pp; Japanese.
PS XX	CC XX	The invention relates to a method of treating a cancer patient by administering cancer antigens to patient, involves evaluating presence or absence of specific cytotoxic T-lymphocyte precursors for individual peptides contained in set of cancer antigen peptides, in patient, removing peptide being non-specific to precursors, from cancer antigen peptide set, to prepare set for administration, and administering cancer antigen peptide set to patient. The method is useful for treating cancer patient by administering cancer antigens to patient. The present sequence represents the amino acid sequence of a lck peptide cancer antigen.
XX	CC XX	Example 1; SEQ ID NO 3; 36pp; Japanese.
PS XX	CC XX	The invention relates to a method of treating a cancer patient by administering cancer antigens to patient, involves evaluating presence or absence of specific cytotoxic T-lymphocyte precursors for individual peptides contained in set of cancer antigen peptides, in patient, removing peptide being non-specific to precursors, from cancer antigen peptide set, to prepare set for administration, and administering cancer antigen peptide set to patient. The method is useful for treating cancer patient by administering cancer antigens to patient. The present sequence represents the amino acid sequence of a lck peptide cancer antigen.
XX	CC XX	Query Match 100.0%; Score 50; DB 10; Length 9;
SQ Sequence 9 AA;	CC XX	Best Local Similarity 100.0%; Pred. No. 2.1e+06; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYTNASDGL 9	CC XX	Db 1 HYTNASDGL 9
Db 1 HYTNASDGL 9	AC XX	
AC ADN11799;	XX XX	RESULT 8
XX XX	ID XX	ADN11799 standard; protein; 98 AA.
AC XX	AC XX	ADN11799;
XX XX	DT XX	17-JUN-2004 (first entry)
SQ Sequence 9 AA;	DE XX	Lck SH2 domain, SEQ ID 5.
QY 1 HYTNASDGL 9	KW XX	Cytostatic; SH2-phosphorylated ligand complex; SH2-like domain; signaling protein; chronic myelogenous leukaemia; CML; acute lymphocytic leukaemia; ALL; SH2 domain; Lck.
Db 1 HYTNASDGL 9	KW XX	Unidentified.
AC XX	OS XX	CA2417838-A1.
AC AEE99213;	PN XX	01-MAY-1993.
ID AEE99213 standard; peptide; 9 AA.	PD XX	31-OCT-1991; 9ICA-02417838.
XX XX	PR PR	31-OCT-1991; 9ICA-02054602.
RESULT 7		
ID AEE99213		



XX PT Method for inhibiting or reducing signal transduction - utilises peptide  
 PT or corresp. nucleic acid which decreases association of PI 3- or 4-  
 PT kinase with CD4/p56lck.  
 XX PS Disclosure; Page 29-30; 46pp; English.

CC In order for certain T cells to make an optimal response to antigen, it  
 CC is necessary for the T cell surface antigen CD4 to couple to the protein-  
 tyrosine kinase p56lck. (CD4-p56lck is known to associate with and  
 functionally synergise with the Tcr/CD3 complex.) CD4-p56lck complex in T  
 CC cells associates with two lipid kinases: PI 3-kinase and PI 4-kinase,  
 CC which suggests that these lipid kinases are also involved in  
 intracellular signalling via the T cell receptor complex. The interaction  
 CC of a lipid kinase, such as PI 3-kinase or PI 4- kinase, with CD4-p56lck,  
 CC may be blocked by administering a peptide. This peptide may be a fragment  
 CC of the cytoplasmic domain of CD4 (eg AAR60987-R60991), a fragment of  
 CC p56lck (eg AAR60992, AAR60993), a fragment of PI 3-kinase (eg AAR60994,  
 CC AAR60995), or a fragment of PI 4-kinase. Other proline-rich peptides that  
 CC bind to SH3 binding sequences can also be used, such as the fragment of  
 CC 3BPI protein that binds to the SH3 of the Ab1 kinase (AAR60997), or a  
 CC sequence found in the SOS protein (AAR60999). (Updated on 25-MAR-2003 to  
 CC correct PN field.)

CC Revised record issued on 21-OCT-2004 : Correction to feature table key  
 XX SQ Sequence 102 AA;

Query Match 100.0%; Score 50; DB 2; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9  
 Db 77 HYTNASDGL 85

RESULT 11

ID AAR72090 standard; protein; 102 AA.  
 XX AC AAR72090;  
 XX DT 27-SEP-1995 (first entry)  
 DE DET1-DET2-spacer-ek-lck SH2 construct.  
 XX KW Polymerase chain reaction; PCR; amplify; primer; chicken; src;  
 KW SH2 domain; DET1; DET2; erythropoiesis; anaemia; haematopoiesis;  
 KW antagonist.  
 XX OS Synthetic.  
 XX PN EP728482-A2.  
 XX PD 28-AUG-1996.  
 XX PF 07-FEB-1996; 96EP-00200269.  
 XX PR 10-FEB-1995; 95US-00386381.  
 PR 07-MAR-1995; 95US-00400220.  
 PR 30-JUN-1995; 95US-00497357.  
 PR 11-OCT-1995; 95US-00540680.  
 PR 29-DEC-1995; 95US-00581089.

XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX PI Dunnington DJ;  
 XX PN WO9508629-A1.  
 XX PD 30-MAR-1995.  
 XX PT Use of selective antagonist of haematopoietic acid phosphatase SH2 domain  
 PT - with no significant affinity for other SH2 domains, to increase  
 PT erythropoiesis and haematopoiesis, esp. for treatment of anaemia.  
 XX PS Example 3; Page 28-29; 46pp; English.

CC This sequence represents the DET1-DET2-spacer-ek-lck SH2 construct  
 CC encoded by the sequence amplified by the primers given in AAT37297-98.  
 CC This protein fragment was used in the isolation of a compound for  
 CC improving erythropoiesis. The compound may be used for the treatment of  
 CC anaemia or to enhance haematopoiesis. The isolated compound antagonises  
 CC the hcp SH2 domain without side effects caused by non-specific inhibition  
 CC of other SH2 domains  
 XX SQ Sequence 134 AA;

PT genes - useful in drug screening assays and/or for treating cellular  
 PT degradations, derangements and/or dysfunctions, etc.  
 PT XX PS Example 6; Page 117; 160pp; English.

CC A fragment encoding the human Stat91 protein was used to screen a murine  
 CC thymus and spleen cDNA for homologous proteins. A highly homologous gene  
 CC (given in AAQ89338) was isolated that encoded a 91 kDa protein (AAR72080)  
 CC (Stat1) that was responsive to interferon-gamma. The SH2 region of Stat1  
 CC showed homology to SH2 regions of src, Ab1, lck and p85-alpha-N (AAR72088  
 CC -91, respectively). (Updated on 25-MAR-2003 to correct PN field.)  
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 102 AA;

Query Match 100.0%; Score 50; DB 2; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9  
 Db 83 HYTNASDGL 91

RESULT 12

ID AAW03982 standard; peptide; 134 AA.  
 XX AC AAW03982;  
 XX DT 30-APR-1997 (first entry)  
 DE DET1-DET2-spacer-ek-lck SH2 construct.  
 XX KW Polymerase chain reaction; PCR; amplify; primer; chicken; src;  
 KW SH2 domain; DET1; DET2; erythropoiesis; anaemia; haematopoiesis;  
 KW antagonist.  
 XX OS Synthetic.  
 XX PN EP728482-A2.  
 XX PD 28-AUG-1996.  
 XX PF 07-FEB-1996; 96EP-00200269.  
 XX PR 10-FEB-1995; 95US-00386381.  
 PR 07-MAR-1995; 95US-00400220.  
 PR 30-JUN-1995; 95US-00497357.  
 PR 11-OCT-1995; 95US-00540680.  
 PR 29-DEC-1995; 95US-00581089.

XX PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX PI Dunnington DJ;  
 XX DR WPI; 1996-386024/39.

XX PT Use of selective antagonist of haematopoietic acid phosphatase SH2 domain  
 PT - with no significant affinity for other SH2 domains, to increase  
 PT erythropoiesis and haematopoiesis, esp. for treatment of anaemia.  
 XX PS Example 3; Page 28-29; 46pp; English.

CC This sequence represents the DET1-DET2-spacer-ek-lck SH2 construct  
 CC encoded by the sequence amplified by the primers given in AAT37297-98.  
 CC This protein fragment was used in the isolation of a compound for  
 CC improving erythropoiesis. The compound may be used for the treatment of  
 CC anaemia or to enhance haematopoiesis. The isolated compound antagonises  
 CC the hcp SH2 domain without side effects caused by non-specific inhibition  
 CC of other SH2 domains  
 XX SQ Sequence 134 AA;

Query Match 100.0%; Score 50; DB 2; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 0.077; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; OS

QY	1 HYTNASDGL 9
Db	112 HYTNASDGL 120

**RESULT 13**

AAW02120	XX
ID AAW02120	Sequence 134 AA:
XX	
AC AAW02120;	
XX	
DT 28-OCT-1996	(first entry)
XX	
DE DET1-DET2-spacer-ek-lck SH2 construct.	
XX	
KW Bone resorption disease; osteoporosis; src SH2 domain antagonist;	
KW src homology 2 domain; lck SH2 domain.	
XX	
OS Homo; sapiens.	
OS Synthetic.	
XX	
FH Key 2. .12	
FT Region /label= DET1	/note= "defined epitope tag from HIV-1 gp120/160"
FT Region 13. .18	
FT /label= DET2	
FT /note= "hexahistidine tag"	
FT Region 19. .21	
FT /label= Spacer	
FT Region 22. .26	
FT /label= EX	
FT /note= "enterokinase cleavage site"	
FT Domain 27. .130	
FT /label= lck-SH2_domain	
XX	
PN EP727211-A1.	
XX	
PD 21-AUG-1996.	
XX	
PF 07-FEB-1996; 96EP-00200270.	
XX	
PR 10-FEB-1995; 95US-00386381.	
PR 07-MAR-1995; 95US-00400220.	
PR 30-JUN-1995; 95US-00497357.	
PR 11-OCT-1995; 95US-00541080.	
PR 29-DEC-1995; 95US-00580868.	
XX	
PA (SMIK ) SMITHKLINE BEECHAM CORP.	
XX	
PI Dunnington DJ;	
XX	
DR WPT; 1996-372674/38.	
XX	
PT Use of selective src SH2 domain ligand - to prepare medicament for	
PT treating bone resorption disease.	
XX	
PS Example 11; Page 28-29; 47pp; English.	
XX	
CC Construct DET1-DET2-spacer-ek-lck SH2 (AAW02120) was obtd. by inserting a	
CC PCR fragment (see also AAT36190-91) coding for human lck SH2 domain into	
CC a vector contg. a tagged chicken src gene DET1-DET2-spacer-SH2 (see also	
CC AAT36186-87). The construct can be expressed in E. coli and used,	
CC together with similar constructs (see also AAW02119-21 and AAW02124-27),	
CC in binding assays to determine the specificity of cpds. to inhibit SH2	
CC domains; cpds. that selectively inhibit the human src SH2 domain are	
CC useful in treating bone resorption diseases such as osteoporosis	
XX	
CC AAW11285-WL1288 represent fusion proteins containing Src homology 2 (SH2)	
CC domains. These sequences are used to identify a compound that targets the	
CC human Stat (signal transduction and activation of transcription) 6 SH2	
CC domain. The identified compounds have a binding affinity for Stat 6 over	
CC 50 (preferably 100) times higher than its affinity for the human Stat 5	
CC SH2 domain. The compound has an affinity for hcp SH2, SH-PTP2 SH2, p85	
CC SH2', Grb2 SH2, src SH2, lck SH2 or fyn SH2 of more than 50 (preferably	
CC 100) times lower than its affinity for Stat 6 SH2. SH2 domains are	

CC conserved non-catalytic sequences found in a variety of signalling  
 CC molecules, such as non-receptor protein tyrosine kinases, and in  
 oncogenic proteins. The compounds identified using the fusion proteins  
 are used as the administered compound in the method of the invention for  
 treating allergic reactions. Administration of the compound avoids the  
 side effects (e.g. reduced erythrocyte production) associated with non-  
 selective inhibition of SH2 domains. Selective compounds can be  
 identified in competitive binding assays using only a small subset (the  
 domains specified above) of SH2 domains rather than all 60 known domains.  
 The method can be used for the treatment of asthma and allergic rhinitis,  
 but can also be used to treat atopic dermatitis. Inhibition of the human  
 CC Stat 6 SH2 domain blocks up-regulation of the IgE receptor mediated by  
 CC interleukin-4 (IL-4) or IL-13  
 XX Sequence 134 AA;  
 Query Match 100.0%; Score 50; DB 2; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 0.077;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYTNASDGL 9  
 Db 112 HYTNASDGL 120

RESULT 15  
 AAW19624  
 ID AAW19624 standard; protein; 134 AA.  
 XX  
 AC AAW19624;  
 DT 27-OCT-1997 (first entry)  
 XX  
 DE Human lck SH2 domain fusion protein.  
 XX  
 KW Stat 5; Signal Transduction and Activation of Transcription;  
 KW Src homology domain; SH2; erythropoiesis enhancing; anaemia;  
 KW fusion protein; ek; enterokinase; epitope; antibody production;  
 KW detection; HIV; human immunodeficiency virus type 1; gp120;  
 KW glycoprotein 120; selective.  
 XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers  
 FT Peptide 2. .12 /note= "defined epitope tag 1 from HIV gp120"  
 FT Peptide 13. .18 /note= "hexahistidine sequence tag"  
 FT Region 19. .21 /label= spacer  
 FT Cleavage-site 22. .26 /note= "enterokinase protease recognition site"  
 FT Peptide 27. .134 /note= "lck SH2"  
 XX  
 PN WO9702024-A1.  
 XX  
 PD 20-MAR-1997.  
 XX  
 PF 11-SEP-1996; 96WO-US014567.  
 XX  
 PR 15-SEP-1995; 95US-0003819P.  
 PR 12-MAR-1996; 96GB-00005210.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Marcy A, Salowe SP, Wisniewski D;  
 XX  
 WPI; 1997-202171/18.  
 DR N-PSDB; AAT63421.  
 XX  
 PT Screening compounds for binding to fusion proteins with defined ligands -  
 PT allows high capacity assays and identification of (ant) agonists or  
 PT inhibitors for drug development.  
 XX  
 PS Claim 32; Page 21-22; 36pp; English.

XX  
 CC Novel fusion proteins FKBP-ZAP:SH2, FKBP-SYK:SH2 and FKBP-LCK:SH2  
 CC (AAW14786-88) comprise FK506 binding protein (FKBP) linked via a peptide  
 CC linker to a target protein composed of a multiple signal transduction  
 CC domain, i.e., ZAP:SH2, SYK:SH2 or LCK:SH2. They can be produced in  
 CC transformed host cells, esp. E. coli, using expression vectors with  
 CC fusion protein DNA sequences (AAT63419-21). The fusion proteins are used  
 CC in novel methods utilising microscintillation plate technology for the  
 CC functional assay of ligand binding to a signal transduction domain (i.e.  
 CC SH2). The method is readily adaptable to robotic automation for high  
 CC capacity screening for agonists, antagonists and/or inhibitors for use in  
 CC drug development

XX  
 PT Enhancing erythropoiesis with specific activator of human Stat 5 SH2  
 PT domain - has very low binding affinity to other SH2 domains so free of  
 PT side effects, particularly for treating anaemia.

XX  
 PS Example 11; Page 54-55; 91pp; English.  
 XX  
 CC AAW19624 is a fusion protein of formula DET1-DET2-Sp-ek-SH2, where DET1  
 CC is a defined epitope tag from HIV-1 gp120, DET2 is a hexahistidine  
 CC sequence tag (binds to nickel-containing resins, used for purification),  
 CC Sp is a spacer, ek is an enterokinase protease recognition site and SH2  
 CC is the human lck SH2 domain. DET1 is included so that antibodies against  
 CC the epitope can be used to detect the recombinant expression of the  
 CC fusion protein and hence the SH2 domain. The fusion proteins are used for  
 CC identifying compounds that bind the SH2 domain causing its activation  
 XX SQ Sequence 134 AA;  
 Query Match 100.0%; Score 50; DB 2; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 0.077;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYTNASDGL 9  
 Db 112 HYTNASDGL 120

RESULT 16  
 AAW14788  
 ID AAW14788 standard; protein; 224 AA.  
 XX  
 AC AAW14788;  
 XX  
 DT 20-JUN-1997 (first entry)  
 XX  
 DE FKBP-LCK:SH2 fusion protein.  
 XX  
 FKBP-LCK:SH2; FK506 binding protein; SH2 domain; Src homology 2;  
 KW fusion protein; high throughput assay; signal transduction; ligand;  
 KW microscintillation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9710253-A1.  
 XX  
 PD 20-MAR-1997.  
 XX  
 PF 11-SEP-1996; 96WO-US014567.  
 XX  
 PR 15-SEP-1995; 95US-0003819P.  
 PR 12-MAR-1996; 96GB-00005210.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Marcy A, Salowe SP, Wisniewski D;  
 XX  
 WPI; 1997-202171/18.  
 DR N-PSDB; AAT63421.

XX  
 PT Screening compounds for binding to fusion proteins with defined ligands -  
 PT allows high capacity assays and identification of (ant) agonists or  
 PT inhibitors for drug development.  
 XX  
 PS Claim 32; Page 21-22; 36pp; English.

XX  
 CC Novel fusion proteins FKBP-ZAP:SH2, FKBP-SYK:SH2 and FKBP-LCK:SH2  
 CC (AAW14786-88) comprise FK506 binding protein (FKBP) linked via a peptide  
 CC linker to a target protein composed of a multiple signal transduction  
 CC domain, i.e., ZAP:SH2, SYK:SH2 or LCK:SH2. They can be produced in  
 CC transformed host cells, esp. E. coli, using expression vectors with  
 CC fusion protein DNA sequences (AAT63419-21). The fusion proteins are used  
 CC in novel methods utilising microscintillation plate technology for the  
 CC functional assay of ligand binding to a signal transduction domain (i.e.  
 CC SH2). The method is readily adaptable to robotic automation for high  
 CC capacity screening for agonists, antagonists and/or inhibitors for use in  
 CC drug development

SQ	Sequence 224 AA;	Db	206 HYTNASDGL 214
Query Match	100.0%; Score 50; DB 2; Length 224;	RESULT 18	
Best Local Similarity	100.0%; Pred. No. 0.14; 0; Mismatches 0; Indels 0; Gaps 0;	ABR59690	
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ID ABR59690 standard; protein; 363 AA.	
QY	1 HYTNASDGL 9	XX AC ABR59690;	
Db	206 HYTNASDGL 214	XX DT 25-JUL-2003 (first entry)	
RESULT 17			
AAW96823			
ID AAW96823	standard; protein; 224 AA.		
XX AC AAW96823;			
XX DT 21-APR-1999 (first entry)			
XX DE A fusion protein of FKBP-Lck.			
XX KW Fusion protein; FK506 binding protein; FKBP; SH2 domain; human Lck; screening; protein binding; ligand-protein interaction; protein-protein interaction; protease inhibitor.			
XX OS Synthetic.			
OS Homo sapiens.			
XX PN WO2003029277-A2.			
XX PD 10-APR-2003.			
XX PF 02-OCT-2002; 2002WO-US031618.			
XX PR 03-OCT-2001; 2001US-0327212P.			
XX PA (RIGE-) RIGEL PHARM INC.			
XX PI Chu P, Li C, Liao XC, Masuda E, Pardo J, Zhao H; DR 2003-363276/34.			
XX DR N-PSDB; ACC81082.			
XX PT Identifying a compound that modulates T lymphocyte activation, useful for monitoring changes in cell surface marker expression, comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound.			
XX DR N-PSDB; AAX15151.			
XX PS Disclosure; Page 64; 126pp; English.			
PT High throughput screening assay - for screening compounds capable of binding to a fusion protein consisting of, e.g., a target protein and an FKS06-binding protein.			
PT Disclosure; Page 26; 42pp; English.			
XX CC The present sequence represents a fusion protein comprising FK506 binding protein (FKBP) and the SH2 domain of human Lck. The protein is used to exemplify the method of the invention. The specification describes a method for screening for compounds capable of binding to a fusion protein. The method comprises mixing a test compound, a biotinylated ligand, the fusion protein, a donor-labelled ligand and acceptor-labelled streptavidin, incubating the mixture, measuring the time-resolved fluorescence attributable to the binding of the biotinylated ligand to the fusion protein in the presence of the test compound and determining the binding of the biotinylated ligand to the fusion protein in the presence of the test compound relative to a control assay run in the absence of the test compound. The methods may be used to determine if compounds are capable of binding to a protein or are capable of blocking ligand-protein or protein-protein interactions. They may be used to identify compounds which are protease inhibitors			
XX SQ Sequence 224 AA;			
Query Match 100.0%; Score 50; DB 2; Length 224;			
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Mismatches 0; Indels 0; Gaps 0;			
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 HYTNASDGL 9			
QY 1 HYTNASDGL 9			
Query Match 100.0%; Score 50; DB 6; Length 363;			
Best Local Similarity 100.0%; Pred. No. 0.23; 0; Mismatches 0; Indels 0; Gaps 0;			
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
SQ Sequence 363 AA;			
Query Match 100.0%; Score 50; DB 6; Length 363;			
Best Local Similarity 100.0%; Pred. No. 0.23; 0; Mismatches 0; Indels 0; Gaps 0;			
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 HYTNASDGL 9			

Db ||||| HYTNASDGL 216

RESULT 19  
ADP48375  
ID ADP48375 standard; protein; 363 AA.  
AC  
XX  
DT 09-SEP-2004 (first entry)  
DE Human lymphocyte specific tyrosine kinase (Lck) polypeptide #2.  
KW Human; lymphocyte specific tyrosine kinase; Lck;  
antisense oligonucleotide; phosphorothioate linkage;  
2'-O-methoxyethyl sugar moiety; 5-methylcytosine;  
hyperproliferative disorder; cancer; cytostatic; enzyme.  
OS Homo sapiens.  
XX  
PN US2004116365-A1.  
XX  
PD 04-JUL-2002.  
XX  
PF 13-MAR-2001; 2001US-00805020.  
XX  
PR 14-MAR-2000; 2000IL-00135402.  
PR 16-MAY-2000; 2000IL-00136154.  
XX  
PA (LEVI/) LEVINE Z.  
PA (DAVI/) DAVID A.  
PA (ROMA/) ROMANO C.  
PA (BERN/) BERNSTEIN J.  
XX  
PI Levine Z, David A, Romano C, Bernstein J;  
XX  
DR WPI; 2002-635679/68.  
XX  
DR N-PSDB; ABS65202.  
XX  
PS Novel nucleic acid sequence, which is an alternative splicing variant of  
PT tumor involved genes, useful for detecting cancer, predisposition to  
PT cancer, for evaluating cancer state and in gene therapy for treating  
PT cancer.  
XX  
PS Claim 4; Page 68-69; 180pp; English.  
XX  
CC The invention discloses isolated human nucleic acid alternative splicing  
variants that are all tumour-involved genes (TRGs). The nucleic acids and  
CC polypeptides are useful for determining the level of a nucleic acid or  
CC polypeptide in a biological sample, for detecting a variant nucleic acid  
or polypeptide sequence in a biological sample, for determining the level  
CC of variant nucleic acid or polypeptide sequences in a biological sample  
and for determining the ratio between the level of variant sequence in a  
CC first biological sample and the level of the original sequence from which  
CC the variant has been varied by alternative splicing in a second  
CC biological sample and for raising antibodies. A pharmaceutical  
composition comprising a carrier and the nucleic acid, is useful for  
treating diseases (e.g. cancer) that can be ameliorated or cured by  
increasing or decreasing the level of the encoded protein. The nucleic  
CC acids are also useful for diagnostic purposes, especially for detecting  
CC cancer or a predisposition to cancer, for evaluating the state or  
CC aggressiveness of cancer disease, in basic research, for understanding  
CC the physiological function of the original TRG, in targeting or  
CC developing pharmaceuticals, for distinguishing various stages in the life  
CC cycle of the same type of cells which may be helpful for the development  
CC of pharmaceuticals for various cancer stages in which cell cycle is non-  
normal, for determining mutations in tumour-involved genes and in gene  
CC therapy. The polypeptides are useful for identifying compounds capable of  
binding to the variant product and modulating its activity and for  
modulating endothelial differentiation and proliferation, as well as to  
CC modulate apoptosis either ex vivo or in vivo. The sequences presented in  
CC ABC796700-ABG79705 are the new variants (NV) 1-36 proteins of the TRGs  
disclosed  
XX  
SQ Sequence 363 AA;

Query Match 100.0%; Score 50; DB 8; Length 363;  
Best Local Similarity 100.0%; Pred. No. 0.23; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTNASDGL 9  
Db ||||| HYTNASDGL 216

RESULT 20  
ABG79672  
ID ABG79672 standard; protein; 437 AA.  
XX  
AC  
XX  
DT 15-NOV-2002 (first entry)  
DE Tumour involved gene (TRG) splice variant protein, NV-3.  
KW Human; splice variant; tumour-involved gene; TRG;  
pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;  
endothelial cell; cell differentiation; cell proliferation; apoptosis;  
gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2002086384-A1.  
XX  
PD 04-JUL-2002.  
XX  
PF 13-MAR-2001; 2001US-00805020.  
XX  
PR 14-MAR-2000; 2000IL-00135402.  
PR 16-MAY-2000; 2000IL-00136154.  
XX  
PA (LEVI/) LEVINE Z.  
PA (DAVI/) DAVID A.  
PA (ROMA/) ROMANO C.  
PA (BERN/) BERNSTEIN J.  
XX  
PI Levine Z, David A, Romano C, Bernstein J;  
XX  
DR WPI; 2002-635679/68.  
XX  
DR N-PSDB; ABS65202.  
XX  
PS Novel nucleic acid sequence, which is an alternative splicing variant of  
PT tumor involved genes, useful for detecting cancer, predisposition to  
PT cancer, for evaluating cancer state and in gene therapy for treating  
PT cancer.  
XX  
PS Claim 4; Page 68-69; 180pp; English.  
XX  
CC The invention discloses isolated human nucleic acid alternative splicing  
variants that are all tumour-involved genes (TRGs). The nucleic acids and  
CC polypeptides are useful for determining the level of a nucleic acid or  
CC polypeptide in a biological sample, for detecting a variant nucleic acid  
or polypeptide sequence in a biological sample, for determining the level  
CC of variant nucleic acid or polypeptide sequences in a biological sample  
and for determining the ratio between the level of variant sequence in a  
CC first biological sample and the level of the original sequence from which  
CC the variant has been varied by alternative splicing in a second  
CC biological sample and for raising antibodies. A pharmaceutical  
composition comprising a carrier and the nucleic acid, is useful for  
treating diseases (e.g. cancer) that can be ameliorated or cured by  
increasing or decreasing the level of the encoded protein. The nucleic  
CC acids are also useful for diagnostic purposes, especially for detecting  
CC cancer or a predisposition to cancer, for evaluating the state or  
CC aggressiveness of cancer disease, in basic research, for understanding  
CC the physiological function of the original TRG, in targeting or  
CC developing pharmaceuticals, for distinguishing various stages in the life  
CC cycle of the same type of cells which may be helpful for the development  
CC of pharmaceuticals for various cancer stages in which cell cycle is non-  
normal, for determining mutations in tumour-involved genes and in gene  
CC therapy. The polypeptides are useful for identifying compounds capable of  
binding to the variant product and modulating its activity and for  
modulating endothelial differentiation and proliferation, as well as to  
CC modulate apoptosis either ex vivo or in vivo. The sequences presented in  
CC ABC796700-ABG79705 are the new variants (NV) 1-36 proteins of the TRGs  
disclosed  
XX  
SQ Sequence 437 AA;

Query Match 100.0%; Score 50; DB 5; Length 437;  
Best Local Similarity 100.0%; Pred. No. 0.29; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTNASDGL 9  
Db ||||| HYTNASDGL 216

Db 208 HYTNASDGL 216  
 RESULT 21  
 AAB37700  
 ID AAB37700 standard; protein; 508 AA.  
 XX  
 AC  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Human lymphocyte kinase.  
 KW Human; lymphocyte kinase; protein co-ordinate data; lck; crystal.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN WO200070030-A1.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 19-MAY-2000; 2000WO-US013881.  
 XX  
 PR 19-MAY-1999; 99US-0134965P.  
 XX  
 PT (KINE-) KINETIX PHARM INC.  
 XX  
 PI Zhu X;  
 XX  
 DR WPI; 2000-687708/67.  
 XX  
 PT Crystal of a protein-ligand complex for identifying kinase inhibitors,  
 PT comprises a truncated lymphocyte kinase and a ligand, and diffracts X-  
 PT rays to determine atomic coordinates at a resolution greater than 5  
 PT angstroms.  
 XX  
 PS Claim 1; Page 434-5; 438pp; English.  
 XX  
 CC The present invention relates to a crystal of a protein-ligand complex  
 CC comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal  
 CC diffracts X-rays so that the atomic coordinates of the protein-ligand  
 CC complex can be determined to a resolution of greater than 5.0 Angstroms.  
 CC The truncated lck used in the present invention comprises the globular  
 CC core of the corresponding full-length lck. The present sequence is the  
 CC full-length human lck protein. The crystal of the present invention may  
 CC be used to identify kinase inhibitors in screening assays, in drug  
 CC screening and drug design processes, to design, select or test inhibitors  
 CC of kinase enzymes, where the inhibitors are used as therapeutics for the  
 CC treatment and modulation of diseases, disease symptoms or the effect of  
 CC other physiological events mediated by kinases, having one or more kinase  
 CC enzymes involved in their pathology  
 XX  
 SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 3; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9  
 Db 207 HYTNASDGL 215

RESULT 22  
 ADE58802  
 ID ADE58802 standard; protein; 508 AA.  
 XX  
 AC ADE58802;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Protein P06239, SEQ ID NO 4689.

Db 208 HYTNASDGL 216  
 KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX  
 OS Homo sapiens.  
 PN WO2003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.  
 DR GENBANK; P06239.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polyrnucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9  
 Db 207 HYTNASDGL 215

RESULT 23  
 ADE58799  
 ID ADE58799 standard; protein; 508 AA.  
 XX  
 AC ADE58799;

XX  
 DT 29-JAN-2004 (first entry)  
 XX DE Human Protein P06239, SEQ ID NO 4686.  
 XX KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX OS Homo sapiens.  
 PN WO2003016475-A2.  
 XX PD 27-FEB-2003.  
 XX PR 14-AUG-2002; 2002WO-US025765.  
 XX PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX DR WPI; 2003-268312/26.  
 XX DR GENBANK; P06239.  
 XX PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX PS Claim 1; Page; 1017pp; English.  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 comprising the vector, a method for identifying a nucleotide sequence  
 which is differentially regulated in an animal subjected to pain and a  
 kit to perform the method, an array, a method for identifying an agent  
 that increases or decreases the expression of the polynucleotide sequence  
 that is differentially expressed in neuronal tissue of a first animal  
 subjected to pain, a method for identifying a compound which regulates  
 the expression of a polynucleotide sequence which is differentially  
 expressed in an animal subjected to pain, a method for identifying a  
 compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 activity in an animal of one or more of the polypeptides given in the  
 specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 7; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25  
 QY 1 HYTNASDGL 9  
 Db 207 HYTNASDGL 215

ADL34479  
 ID ADL34479 standard; peptide; 508 AA.  
 XX AC ADL34479;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Human lymphocyte kinase (Lck) globular core.  
 XX KW cytostatic; immunosuppressive; antiinflammatory; antibacterial; virucide;  
 KW fungicide; nootropic; neuroprotective; kinase inhibitor; crystal;  
 KW protein-ligand complex; Lymphocyte kinase; Lck; Lck ligand;  
 KW kinase inhibitor; therapeutic; kinase-mediated physiological event;  
 KW cancer; autoimmunological; metabolic; inflammatory; infection;  
 KW central nervous system degenerative disease; transplant rejection; human;

XX Query Match 100.0%; Score 50; DB 7; Length 508;  
 XX Best Local Similarity 100.0%; Pred. No. 0.34;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYTNASDGL 9  
 Db 207 HYTNASDGL 215

ADL34479  
 ID ADL34479 standard; peptide; 508 AA.  
 XX AC ADL34479;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Human lymphocyte kinase (Lck) globular core.

RESULT 24  
 ID ADF45072  
 ID ADF45072 standard; protein; 508 AA.  
 XX AC ADF45072;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE Human kinase LCK.  
 XX KW Human; protein kinase; enzyme; inhibitor; LCK.  
 XX OS Homo sapiens.

PN WO2003081210-A2.  
 XX PD 02-OCT-2003.  
 XX PR 20-MAR-2003; 2003WO-US008725.  
 PR 21-MAR-2002; 2002US-0366892P.  
 XX PA (SUNE-) SUNESIS PHARM INC.  
 XX PI Prescott JC, Braisted A;  
 XX DR WPI; 2003-865136/80.  
 XX PT Identifying ligand binding to inactive conformation of target protein  
 PT kinase (T) comprises contacting the conformation modified (T') which  
 PT contains reactive group at binding site, with ligands and detecting  
 PT kinase-ligand conjugate formation.

XX PS Disclosure; SEQ ID NO 41; 260pp; English.

CC The present invention relates to a method for identifying a ligand (L),  
 CC which binds to an inactive conformation of target protein kinase (T). The  
 CC method involves contacting inactive conformation of (T'), which contains  
 CC or is modified to contain a reactive group at or near a binding site of  
 CC interest, with one or more ligand candidates capable of covalently  
 CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).  
 CC The method is useful for identifying protein kinase inhibitors that  
 CC preferentially bind to inactive conformation of a target protein kinase.  
 CC The present sequence is a protein kinase which may be modified via an  
 CC amino acid substitution, for use in the method of the invention.

XX SQ Sequence 508 AA;

KW globular core; protein co-ordinate data.

XX KW

OS Homo sapiens.

XX KW

PN antirheumatic; cytostatic; antibacterial; gene therapy; human.

XX OS

PD Homo sapiens.

XX XX

PF 08-JUL-2003.

XX XX

PF 21-MAY-2001; 2001US-00862154.

XX XX

PR 19-MAY-2000; 2000US-0205510P.

XX XX

PA (AMGE-) AMGEN INC.

XX XX

PI Zhu X;

XX XX

DR WPI; 2003-810380/76.

XX XX

PT Crystal of protein-ligand complex useful for identifying an inhibitor of

PT PT

PT Lymphocyte kinase (Lck), comprises truncated Lck and a ligand.

XX XX

PS Claim 1; SEQ ID NO 1; 295pp; English.

XX XX

CC The invention describes a crystal (I) of a protein-ligand complex (C) comprising a truncated lymphocyte kinase (Lck) and a ligand, where (I) effectively diffracts X-rays for determination of atomic coordinates of (C) to a resolution of greater than 5.0 angstroms, and truncated Lck comprises a sequence (S1) of residues 225-508 of a 508 amino acid sequence, given in specification and retains the globular core of full length Lck. (I) is useful in an inhibitor screening assay and to identify, design, select, and evaluate potential inhibitors of kinases that would be useful as therapeutics for diseases or symptoms of diseases that are associated with kinase-mediated physiological events. The inhibitors identified by the methods may also be useful for inhibition of kinase activity of one or more enzymes. The inhibitors are also useful for inhibiting the biological activity of any enzyme comprising greater than 90%, alternatively greater than 85%, or alternatively greater than 70% homology with a kinase sequence. The inhibitors are useful for inhibiting the biological activity of any enzyme that binds ATP and thus for treating disease or disease symptoms mediated by any enzyme that binds ATP. The inhibitors are useful in inhibiting kinase activity and are useful in treating kinase-mediated disease or disease symptoms in a mammal, particularly a human e.g., cancer, autoimmunological, metabolic, inflammatory, infection, (bacterial, viral, yeast, fungal, etc.), central nervous system degenerative disease etc. The inhibitors are useful in treating or preventing diseases, including, transplant rejection etc. This is the amino acid sequence of a human lymphocyte kinase (Lck) polypeptide comprising the Lck globular core.

XX XX

SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 7; Length 508;  
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTNASDGL 9  
Db 207 HYTNASDGL 215

RESULT 26

ADS8148 ID ADS8148 standard; protein; 508 AA.

XX XX

AC ADS8148;

DT 18-NOV-2004 (first entry)

DE Human protein of a TNF-alpha signalling pathway SeqID 3.

XX XX

KW protein complex; tumour necrosis factor-alpha signalling pathway; TNF-alpha; chronic inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; infectious disease; septic shock;

KW bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic;

XX KW

OS Homo sapiens.

XX OS

PD Homo sapiens.

XX XX

PF WO2004035783-A2.

XX XX

PF 29-APR-2004.

XX XX

PR 24-SEP-2003; 2003WO-EP050655.

XX XX

PR 26-SEP-2002; 2002EP-00021809.

XX XX

PR 10-FEB-2003; 2003EP-00100274.

XX XX

PA (CELL-) CELLZONE AG.

XX XX

PT Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;

PI Superti-Furga G, Kruse U;

DR WPI; 2004-348460/32.

XX XX

PT New protein complex comprising at least one first and second protein of the tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for diagnosing or treating inflammation, neurological diseases, infectious diseases or cancer.

XX XX

PS Example; SEQ ID NO 3; 1980pp; English.

CC This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The present invention describes a protein complex and kit that are useful for diagnosing, prognosis or treating chronic inflammatory diseases such as rheumatoid arthritis and inflammatory bowel disease; infectious diseases such as septic shock and bacterial infections; neurological diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirheumatic, cytostatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides siRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification to form novel complexes of the TNF-alpha signalling pathway of the invention.

XX XX

SQ Sequence 508 AA;

Query Match 100.0%; Score 50; DB 8; Length 508;  
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTNASDGL 9  
Db 207 HYTNASDGL 215

RESULT 27

AY49420 ID AY49420 standard; protein; 509 AA.

XX XX

AC AY49420;

DT 13-MAR-2000 (first entry)

DE PKA substrate, Src-family protein.

XX XX

KW Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer; kinase substrate; immunosuppressive disorder; proliferative disease; HIV infection; AIDS; immunodeficiency; autoimmune disease;

KW	systemic lupus erythematosus; Src-family.
OS	Homo sapiens.
XX	
XX	02-DEC-1999.
PD	27-MAY-1998; 98NO-00002419.
XX	PR 30-DEC-1998; 98US-0114240P.
XX	PA (LAUR-) LAURAS AS.
XX	PA (JONE/) JONES E L.
PI	Hansson V, Levy FO, Mustelin T, Skalhegg BS, Sundvold V;
PI	Tasken K, Vang T, Altman A, Munshi A;
XX	DR WPI; 2000-086801/07.
XX	N-PSDB; AAZ46491.
PT	Altering the activity of protein kinase signaling pathways, used for treating immunosuppressive disorders, e.g. AIDS, proliferative disorders, e.g. cancers or autoimmune diseases.
PT	Claim 23; Page 95-96; 111pp; English.
PS	The invention provides a novel method of altering the activity of the protein kinase A (PKA) signaling pathway in a cell that comprises altering the extent of phosphorylation of one or more PKA substrates, or kinase substrates downstream in the PKA signaling pathway. Pharmaceutical compositions containing a nucleic acid molecule that encodes a PKA substrate, or fragment, precursor or functionally equivalent variant, where the sequence is modified to alter its susceptibility to phosphorylation by PKA can be used for treating a disorder exhibiting abnormal PKA signaling activity, immunosuppressive disorders or proliferative diseases. They can be used for treating e.g. HIV infection, AIDS, common variable immunodeficiency or cancers. Conditions in which upregulation of the PKA pathway is required, such as autoimmune disease, e.g. systemic lupus erythematosus, may also be treated. The present sequence represents a PKA substrate, wherein the substrate is in the Src-family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, c-ckl, Fyk, Src-1 or Src-2
XX	SQ Sequence 509 AA;
Query Match	100.0%; Score 50; DB 3; Length 509;
Best Local Similarity	100.0%; Pred. No. 0.34;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 HYTNASDGL 9
Db	208 HYTNASDGL 216
RESULT 28	ABR58699
ID	ABR58699 standard; protein; 509 AA.
XX	
AC	ABR58699;
XX	09-JUL-2003 (first entry)
DE	Human cancer related protein SEQ ID NO:356.
XX	Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
OS	Homo sapiens.
XX	WO2003025138-A2.
PD	27-MAR-2003.
XX	17-SEP-2002; 2002WO-US029560.
XX	PR 17-SEP-2001; 2001US-0323469P.
XX	PR 20-SEP-2001; 2001US-0323887P.
PR	13-NOV-2001; 2001US-0350666P.
PR	08-FEB-2002; 2002US-0355145P.
PR	08-FEB-2002; 2002US-0355257P.
PR	12-APR-2002; 2002US-0372246P.
XX	PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX	PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI	Zlotnik A;
XX	DR WPI; 2003-354600/33.
DR	N-PSDB; ACC72850.
XX	New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
PT	Claim 12; Page 762; 767pp; English.
PS	The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these pathologies
XX	SQ Sequence 509 AA;
Query Match	100.0%; Score 50; DB 6; Length 509;
Best Local Similarity	100.0%; Pred. No. 0.34;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 HYTNASDGL 9
Db	208 HYTNASDGL 216
RESULT 29	ABR56202
ID	ABR56202 standard; protein; 509 AA.
XX	
AC	ABR56202;
XX	18-DEC-2003 (first entry)
DE	Human Lymphocyte Cell Kinase, Lck.
XX	Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
OS	Homo sapiens.
XX	WO2003020880-A2.

XX  
PD 13-MAR-2003.  
XX  
PF 02-AUG-2002; 2002WO-US024546.  
XX  
PR 03-AUG-2001; 2001US-0310051P.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Borhani DW, Calderwood D, Dixon RW, Hirst GC, Hnchar P, Loew A;  
PI Leung A, Ritter K;  
XX  
DR WPI; 2003-300872/29.  
XX  
PT New crystalline polypeptide comprising ligand binding domain or catalytic domain of Lck protein, for determining three-dimensional structure of catalytic domain of Lck, has predetermined unit cell parameters.  
XX  
PS Claim 5; Fig 1; 994pp; English.

CC The present invention relates to a crystalline polypeptide (I), comprising the catalytic domain of human Lymphocyte Cell Kinase (Lck) protein. Lck is a Src-family protein tyrosine kinase expressed primarily in T-cells and plays an essential role in immune response. The present sequence is the full-length sequence of human Lck (1-509). (I) is useful for identifying a compound which is an inhibitor of human Lck protein

SQ Sequence 509 AA;

Query Match 100.0%; Score 50; DB 7; Length 509;  
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; MisMatches 0;

Qy 1 HYTNASDGL 9  
Db 208 HYTNASDGL 216

RESULT 30  
ADE40449

ID ADE40449 standard; protein; 509 AA.  
XX  
AC ADE40449;  
XX  
DT 29-JAN-2004 (first entry)

DE Human proto-oncogene Tyr protein kinase LCK (gene ID 1611) protein.  
XX  
KW AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;  
KW HIV-related disorder; differential expression; drug screening;  
KW viral replication modulation; diagnosis; prognosis; predisposition;  
KW anti-HIV; gene therapy; antisense therapy; human;  
KW proto-oncogene Tyr protein kinase LCK; enzyme.  
XX  
OS Homo sapiens.  
XX  
PN WO2003070883-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 13-FEB-2003; 2003WO-US004246.

XX  
PR 15-FEB-2002; 2002US-0357391P.  
PR 13-MAY-2002; 2002US-0380249P.  
PR 25-JUN-2002; 2002US-0391306P.  
PR 27-AUG-2002; 2002US-0406297P.  
PR 19-SEP-2002; 2002US-0412007P.  
PR 10-OCT-2002; 2002US-0417508P.  
PR 10-DEC-2002; 2002US-0432318P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Powell DM, Weich NS;

XX DR WPI; 2003-671808/63.  
XX DR N-PSDB; ADE40448.  
XX PT Identifying a compound capable of diagnosing, preventing or treating AIDS or an HIV-related disorder comprises assaying the ability of the compound to modulate e.g. 1414, 1481 or 1553 nucleic acid expression or polypeptide activity.  
XX PT PS Claim 1; SEQ ID NO 28; 167pp; English.

CC The invention relates to a method of identifying a compound useful in the treatment of AIDS (acquired immunodeficiency syndrome) or an HIV (human immunodeficiency virus)-related disorder. The invention involves assaying the ability of a test compound to modulate the activity or expression of 26 human proteins. These proteins and nucleic acids encoding them (ADE40422-ADE40473) are differentially expressed in tissues relating to AIDS or an HIV-related disorder compared to their expression in normal tissues. The invention also relates to the use of the compounds identified to modulate viral replication in a cell and to treat a patient with AIDS or an HIV-related disorder. The invention further discloses methods for the diagnostic evaluation and prognosis of various HIV-related disorders, and for the identification of individuals exhibiting a predisposition to such conditions. The modulatory compounds identified using the method of the invention may be small organic molecules, peptides, antibodies or antisense nucleic acid molecules. The methods of the invention are useful in diagnosing, preventing or treating AIDS or HIV-related disorders. The present sequence represents a human protein which is differentially expressed in AIDS or HIV-related disorders.

XX SQ Sequence 509 AA;

Query Match 100.0%; Score 50; DB 7; Length 509;  
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; MisMatches 0;

Qy 1 HYTNASDGL 9  
Db 208 HYTNASDGL 216

Search completed: June 29, 2006, 09:13:15  
Job time : 90.8313 secs

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OM protein - protein search, using sw model

Run on: June 29, 2006, 08:59:39 ; Search time 105.831 seconds  
 (without alignments)  
 78.664 Million cell updates/sec

Title: US-10-062-257A-3

Perfect score: 50

Sequence: 1 HYTNASDGL 9

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 100 summaries

Database : UniProt\_7.2:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	%
1	50	100.0	368	Q3TLX4_MOUSE	71
2	50	100.0	379	Q4FZR6_RAT	72
3	50	100.0	508	LCK_AOTNA	73
4	50	100.0	508	LCK_HUMAN	74
5	50	100.0	508	LCK_MOUSE	75
6	50	100.0	508	LCK_SAISC	76
7	50	100.0	509	Q7RTZ3_HUMAN	77
8	50	100.0	509	Q95M32_9PRIM	78
9	41	82.0	450	Q73786_XENLA	79
10	40	80.0	193	Q81295_9HEPC	80
11	40	80.0	408	Q4R6L8_MACFA	81
12	40	80.0	505	FRK_HUMAN	82
13	40	80.0	505	Q9NTR5_HUMAN	83
14	40	80.0	509	Q3ZCM0_BOVIN	84
15	39	78.0	323	Q9SH39_ARATH	85
16	39	78.0	324	Q5QE2_ARATH	86
17	38	76.0	276	Q38KH2_BOVIN	87
18	38	76.0	525	Q8AWF1_BRARE	88
19	38	76.0	943	Q7QE10_ANOGA	89
20	38	76.0	1114	Q2PBR5_9VIRU	90
21	37	74.0	351	Q6IJB6_DROME	91
22	37	74.0	358	Q6W9M4_PENMA	92
23	37	74.0	359	Q5DPY8_PARBR	93
24	37	74.0	359	Q2URQ7_ASPOR	94
25	37	74.0	359	Q4WYB0_ASPPU	95
26	37	74.0	360	Q6OQ64_CAEBR	96
27	37	74.0	361	Q9Y7E3_EMENI	97
28	37	74.0	368	Q5B8P0_EMENI	98
29	37	74.0	368	Q4VT41_CAEBR	99
30	37	74.0	405	Q4URA6_XANCB8	100
31	37	74.0	405	Q8PC78_XANCP	101

RESULT 1 "Antisense transcription in the Mammalian Transcriptome.";  
 Q3TLX4\_MOUSE RT  
 ID RN  
 Q3TLX4\_MOUSE PRELIMINARY; PRT; 368 AA.  
 AC  
 ID [4]  
 DT 11-OCT-2005, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, sequence version 1.  
 DE Mammary gland RCB-0526 JYg-MC(A) cDNA, RIKEN full-length enriched library, clone:G830026006 product:lymphocyte protein tyrosine kinase, full insert sequence. (Fragment).  
 DE Name=Lick;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 TISSUE=Mammary gland;  
 MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";  
 RT Methods Enzymol. 303:19-44 (1999).  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Mammary gland;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Lenhard B., Wells C., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Gough J., Frith M.C., Maeda N., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M., Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Hummiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollrias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich D., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuza S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiyra K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.-R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamamoto H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Rida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shirakita T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Ohno Y., Suzuki H., Kawai J., Hayashizaki Y.; "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563 (2005).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 TISSUE=Mammary gland;  
 MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka T., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai J.H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagaawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarella J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 TISSUE=Mammary gland;  
 MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RT Genome Res. 10:1617-1630 (2000).  
 RL [7]  
 RN NUCLEOTIDE SEQUENCE.  
 TISSUE=Mammary gland;  
 MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., [7]

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishime T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuurra S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 [8]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Logue Lano N.A., Peters R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E.,  
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., Smailius D.E.,  
 CC "Generation and initial analysis of more than 15,000 full-length human  
 CC and mouse cDNA sequences."  
 CC proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC [2]

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CC EMBL; AK166263; BAE38668.1; -; mRNA.  
 DR MGI; MGI:96756; Lck.  
 DR GO; GO:004674; F:protein serine/threonine kinase activity; RCA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD00001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00219; TyrKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR ATP-binding; Kinase; Nucleotide-binding; Transferase;  
 KW Tyrosine-protein kinase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 368 AA; 42018 MW; 7AB6AE53AFLA5059 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9  
 Db 67 HYTNASDGL 75

RESULT 2

Q4FZR6\_RAT PRELIMINARY; PRT; 379 AA.

Q4FZR6\_RAT PRELIMINARY; PRT; 379 AA.

AC Q4FZR6;  
 DT 30-AUG-2005, integrated into UniProtKB/TREMBL.  
 DT 30-AUG-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 7.  
 DE lck\_mapped protein (Fragment).  
 GN Name=lck\_mapped;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 [1]

Qy 1 HYTNASDGL 9  
 Db 78 HYTNASDGL 86

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Logue Lano N.A., Peters R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E.,  
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., Smailius D.E.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Thymus;  
 RG NIH MGC Project;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DDJB databases.  
 CC CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 CC tyrosine phosphate.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs license

CC EMBL; BC099218; AAH99218.1; -; mRNA.  
 CC SMR; Q4FZR6; 2-379.

CC DR GO; GO:0005524; F:ATP binding; IEA.  
 CC DR GO; GO:00004713; F:protein-tyrosine kinase activity; IEA.  
 CC DR GO; GO:0016740; F:transferase activity; IEA.  
 CC DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 CC DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 CC DR InterPro; IPR000719; Prot kinase.  
 CC DR InterPro; IPR002290; Ser\_Thr\_pk kinase.  
 CC DR InterPro; IPR000980; SH2.  
 CC DR InterPro; IPR001245; Tyr\_pk kinase.  
 CC DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 CC DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 CC DR Pfam; PF00017; SH2; 1.  
 CC DR PRINTS; PR00401; SH2DOMAIN.  
 CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC DR PROSITE; PS50001; SH2; 1.  
 CC DR SMART; SM00219; TyrKC; 1.  
 CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC DR PROSITE; PS50001; SH2; 1.  
 CC DR SMART; SM00252; SH2; 1.  
 CC DR SMART; SM00219; TyrKC; 1.  
 CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC DR PROSITE; PS50001; SH2; 1.  
 CC DR ATP-binding; Kinase; Nucleotide-binding; Transferase;  
 CC KW Tyrosine-protein kinase.

Query Match 100.0%; Score 50; DB 2; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3	
LCK_AOTNA	STANDARD; PRT: 508 AA.
ID	Q5PKS1;
AC	08-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT	08-NOV-2005, sequence version 3.
DE	Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase).
DR	Name=LCK;
GN	Aotus nancymaae (Ma's night monkey).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX	NCBI_TaxID=37293;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [mRNA].
RA	Perez-Quintero L.A.; Verner J.P.; Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL	-!- FUNCTION: Tyrosine kinase that plays an essential role for the selection and maturation of developing T-cell in the thymus and in mature T-cell function. Is constitutively associated with the cytoplasmic portions of the CD4 and CD8 surface receptors and plays a key role in T-cell antigen receptor (TCR)-linked signal transduction pathways. Association of the TCR with a peptide thereby recruits the associated LCK to the vicinity of the TCR/CD3 complex. LCK then phosphorylates tyrosines residues within the immunoreceptor tyrosines-based activation motifs (ITAMs) in the cytoplasmic tails of the TCRgamma chains and CD3 subunits, initiating the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with the cytoplasmic tail of CD2, and upon engagement of the CD2 molecule, LCK undergoes hyperphosphorylation and activation. Also plays a role in the IL2 receptor-linked signaling pathway that controls T-cell proliferative response. Binding of IL2 to its receptor results in increased activity of LCK. Is expressed at all stages of thymocyte development and is required for the regulation of maturation events that are governed by both pre-TCR and mature alpha beta TCR (By similarity).
CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.
CC	-!- SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KHDRBS1/p70 through its SH2 domain. Interacts with SQSTM1. Interacts with phosphorylated LIME1. Interacts with CB1B (By similarity).
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane. Present in lipid rafts in an inactive form (By similarity). -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1. Interaction is regulated by Ser-58 phosphorylation (By similarity).
CC	-!- SIMILARITY: Belongs to the Tyr protein kinase family. SRC subfamily.
CC	-!- SIMILARITY: Contains 1 SH2 domain.
CC	-!- SIMILARITY: Contains 1 SH3 domain.
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	EMBL; AY821852; AAV70114.2; -; mRNA.
DR	SMR; Q5PKS1; 64-508.
DR	InterPro; IPR00719; Prot_kinase.
DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	InterPro; IPR000980; SH2.
DR	InterPro; IPR01452; SH3.
DR	InterPro; IPR01245; Tyr_pk kinase.
DR	InterPro; IPR008266; Tyr_pk kinase AS.
RESULT 4	
LCK_HUMAN	STANDARD; PRT: 508 AA.
ID	LCK_HUMAN
AC	P06239; P07100; Q12850; Q13152; Q5TDH8; Q5TDH9; Q96DW4; Q9NYT8;
DT	01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT	01-FEB-1994, sequence version 5.
DT	07-MAR-2006, entry version 87.
DE	Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK) (Lymphocyte cell-specific protein-tyrosine kinase) (LSK) (T cell-specific protein-tyrosine kinase).
GN	Name=LCK;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoi.
OC	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [mRNA].
RX	MEDLINE=87133831; PubMed=3493153;
RA	Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y., Mak T.W.;
RT	"A human T cell-specific cDNA clone (Y116) encodes a protein with extensive homology to a family of protein-tyrosine kinases.";

RL Eur. J. Immunol. 16:1643-1646(1986).  
 RN [2] RT  
 RP "Structure of the two promoters of the human lck gene: differential  
 RX accumulation of two classes of lck transcripts in T cells.";  
 MEDLINE=89123626; PubMed=3265417;  
 RL Mol. Cell. Biol. 9:2173-2180(1989).  
 RA [110]  
 RP NUCLEOTIDE SEQUENCE [mRNA] OF 13-508.  
 RA Perlmutter R.M., Marth J.D., Lewis D.B., Peet R., Ziegler S.F.,  
 Wilson C.B.;  
 RT "Structure and expression of lck transcripts in human lymphoid  
 cells.";  
 RL J. Cell. Biochem. 38:117-126(1988).  
 RA [3] RN  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
 RX MEDLINE=90108697; PubMed=2558056; DOI=10.1016/0378-1119(89)90144-3;  
 RA Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,  
 Benarous R.;  
 RT "Structure of the human lck gene: differences in genomic organisation  
 within src-related genes affect only N-terminal exons.";  
 RL Gene 84:105-113(1989).  
 RN [4] RT  
 RP NUCLEOTIDE SEQUENCE [mRNA], VARIANTS LEU-27; GLN-LYS-PRO-231 INS;  
 RC TISSUE=Lymphoma;  
 RT "Oncogenic activation of the lck protein accompanies translocation of  
 the lck gene in the human HSB2 T-cell leukemia.";  
 RL Mol. Cell. Biol. 14:2429-2437(1994).  
 RN [5] RT  
 RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM SHORT), AND ALTERNATIVE SPLICING.  
 RC TISSUE=Leukemic T-cell;  
 RX MEDLINE=94187714; PubMed=8139546;  
 RA Wright D.D., Sefton B.M., Kamps M.P.;  
 RT "An aberrant lck mRNA in two human T-cell lines.";  
 RL Biochim. Biophys. Acta 1264:168-172(1995).  
 RN [6] RT  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RG Human chromosome 1 international sequencing consortium;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.  
 RN [7] RT  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA] (ISOFORM 3).  
 RC TISSUE=Lymph;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnier A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [8] RT  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.  
 RX MEDLINE=89096891; PubMed=2850479;  
 RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.,  
 RT "Structure of the murine lck gene and its rearrangement in a murine  
 lymphoma cell line.";  
 RL Mol. Cell. Biol. 8:3058-3064(1988).  
 RN [9] RT  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.  
 RX MEDLINE=89313764; PubMed=2787474;  
 RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,  
 RA Miyamoto N.G., Mak T.W.;  
 RP REVIEW.  
 RX PubMed=10848956;  
 RA Isakov N., Biesinger B.;  
 RT "Lck protein tyrosine kinase is a key regulator of T-cell activation  
 and a target for signal intervention by Herpesvirus saimiri and other

RT viral gene products.";  
 RL Eur. J. Biochem. 267:3413-3421(2000).  
 RN [19]

RP SUBCELLULAR LOCATION.  
 RX PubMed=12218089;

RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,  
 RA Minaki Y., Kato A., Tani-Ichi S., Hamaoka T., Kosugi A.;  
 RT "Fyn is essential for tyrosine phosphorylation of Csk-binding  
 protein/phosphoprotein associated with glycolipid-enriched  
 microdomains in lipid rafts in resting T cells.";  
 RL J. Immunol. 169:2813-2817(2002).

RN [20]

RP MASS SPECTROMETRY.

RC TISSUE=Mammary cancer;  
 RX MEDLINE=21829512; PubMed=11840567;

RA DOI=10.1002/1615-9861(200202)2:2<212::AID-PROT212>3.0.CO;2-H;  
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brustein L., Herath A.,  
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,  
 RA Zvelebil M.J.;"Cluster analysis of an extensive human breast cancer cell line  
 protein expression map database.";  
 Proteomics 2:212-223(2002).

RN [21]

RP INTERACTION WITH LIME1.  
 RX PubMed=14610046; DOI=10.1084/jem.20031484;

RA Brdickova N., Brdicka T., Angelisova P., Horvath O., Spicka J.,  
 RA Hilgert I., Paces J., Simeoni L., Kliche S., Merten C., Schraven B.,  
 RA Horejsi V.; "LIME: a new membrane raft-associated adaptor protein involved in CD4  
 and CD8 coreceptor signaling.";  
 J. Exp. Med. 198:1453-1462(2003).

RN [22]

RP INTERACTION WITH LIME1.

Query Match 100.0%; Score 50; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 0.23;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 9  
 Db 207 HYTNASDGL 215

---

RESULT 5

LCK\_MOUSE STANDARD PRT; 508 AA.  
 ID LCK\_MOUSE  
 AC P06240; Q61794; Q62320; Q91X65;  
 DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.  
 DT 25-OCT-2005, sequence version 3.  
 DT 07-MAR-2006, entry version 74.

DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)  
 DE (Lymphocyte cell-specific protein-tyrosine kinase) (LSK).  
 GN Name=Lck; Synonyms=Lsk-t;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].  
 RX MEDLINE=86079521; PubMed=2416464; DOI=10.1016/0092-8674(85)90169-2;  
 RA Marth J.D., Peet R., Krebs E.G., Perlmutter R.M.;  
 RT "A lymphocyte-specific protein-tyrosine kinase gene is rearranged and  
 overexpressed in the murine T cell lymphoma LSTRA.";  
 RL Cell 43:393-404(1985).

RN [2]

RP NUCLEOTIDE SEQUENCE [mRNA].  
 RX MEDLINE=861146842; PubMed=3081813;  
 RA Voronova A.F., Sefton B.M.;  
 RT "Expression of a new tyrosine protein kinase is stimulated by  
 retrovirus promoter insertion.";  
 RL Nature 319:682-685(1986).

RN [3]

---

RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].  
 RC STRAIN=FVB/N; TISSUE=salivary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Ronald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [5]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-34.  
 RX MEDLINE=89096891; PubMed=2850479;  
 RA Garvin A.M., Pawar S., Marth J.D., Perlmutter R.M.;  
 RT "Structure of the murine lck gene and its rearrangement in a murine  
 lymphoma cell line.";  
 RL Mol. Cell. Biol. 8:3058-3064 (1988).

RN [16] NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-10.  
 RP RX MEDLINE=88142832; PubMed=3501824;  
 RA RT "Two lck transcripts containing different 5' untranslated regions are  
 present in T cells.";  
 RL Mol. Cell. Biol. 7:4407-4413 (1987).  
 RN [7] MUTAGENESIS OF TYR-504.  
 RP RX MEDLINE=88248001; PubMed=3380790;  
 RA Amrein K.E., Sefton B.M.;  
 "Avian reovirus mRNAs are nonfunctional in infected mouse cells:  
 translational basis for virus host-range restriction.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:4257-4261(1988).  
 RN [8] INTERACTIONS WITH CD4 AND CD8, AND MUTAGENESIS OF 2-CYS--CYS-4; CYS-19  
 AND CYS-22.  
 RP RX MEDLINE=90182665; PubMed=2107025; DOI=10.1016/0092-8674(90)90090-2;  
 RA Turner J.M., Brodsky M.H., Irving B.A., Levin S.D., Perlmutter R.M.,  
 Littman D.R.;  
 "Interaction of the unique N-terminal region of tyrosine kinase p56lck  
 with cytoplasmic domains of CD4 and CD8 is mediated by cysteine motifs.";  
 RT Cell 60:755-765(1990).  
 RN [9] MUTAGENESIS.  
 RP MEDLINE=93059694; PubMed=1279202;  
 RA Hurley T.R., Amrein K.E., Sefton B.M.;  
 RT "Creation and characterization of temperature-sensitive mutants of the  
 lck tyrosine protein kinase.";  
 RL J. Virol. 66:7406-7413(1992).  
 RN [10] MUTAGENESIS OF LYS-272.  
 RP RX MEDLINE=91163633; PubMed=1706070; DOI=10.1038/350062a0;  
 RA Abraham N., Miceli M.C., Parnes J.C., Veillette A.;  
 RT "Enhancement of T-cell responsiveness by the lymphocyte-specific  
 tyrosine protein kinase p56lck.";  
 RL Nature 350:62-66(1991).  
 RN [11] MUTAGENESIS OF TYR-504.  
 RP RX MEDLINE=91219495; PubMed=1708890;  
 RA Abraham K.M., Levin S.D., Marth J.D., Forbush K.A., Perlmutter R.M.;  
 RT "Thymic tumorigenesis induced by overexpression of p56lck.";  
 Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).  
 RN [12] PHOSPHORYLATION BY CSK.  
 RP RX PubMed=8371758; DOI=10.1038/365156a0;  
 RA Chow L.M., Fournel M., Davidson D., Veillette A.;  
 RT "Negative regulation of T-cell receptor signalling by tyrosine protein  
 kinase p50csk.";  
 RL Nature 365:156-160(1993).  
 RN [13] MUTAGENESIS.  
 MEDLINE=93133805; PubMed=8421674;  
 Carrera A.C., Alexandrov K., Roberts T.M.;  
 RT "The conserved lysine of the catalytic domain of protein kinases is  
 actively involved in the phosphotransfer reaction and not required for  
 anchoring ATP.";  
 Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).  
 RN [14] PALMITOYLATION.  
 RP MEDLINE=94019312; PubMed=8413237;  
 RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;  
 RT "Palmitylation of an amino-terminal cysteine motif of protein tyrosine  
 kinases p56lck and p59fyn mediates interaction with glycosyl-  
 RT phosphatidylinositol-anchored proteins.";  
 RL Mol. Cell. Biol. 13:6385-6392(1993).  
 RN [15] PALMITOYLATION.  
 RP MEDLINE=95071286; PubMed=7980442;  
 RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;  
 RT "Palmitoylation of multiple Src-family kinases at a homologous N-  
 terminal motif.";

RL Biochem. J. 303:749-753 (1994).  
 RN [16] INTERACTION WITH CBLB.  
 RP RX PubMed=10646608; DOI=10.1038/35003228;  
 RA Bachmaier K., Krawczyk C., Kozieradzki I., Kong Y.-Y., Sasaki T.,  
 Oliveira-dos-Santos A., Mariathasan S., Bouchard D., Wakeham A.,  
 Itie A., Le J., Ohashi P.S., Sarosi I., Nishina H., Lipkowitz S.,  
 Penninger J.M.;  
 RT "Negative regulation of lymphocyte activation and autoimmunity by the  
 molecular adaptor Cbl-b.";  
 RL Nature 403:211-216(2000).  
 RN [17] SUBCELLULAR LOCATION.  
 RP RX PubMed=12218089;  
 RA Yasuda K., Nagafuku M., Shima T., Okada M., Yagi T., Yamada T.,  
 Minaki Y., Kato A., Tani-Ichi S., Hamaka T., Kosugi A.;  
 RT "Fyn is essential for tyrosine phosphorylation of Csk-binding  
 protein/phosphoprotein associated with glycolipid-enriched  
 microdomains in lipid rafts in resting T cells.";  
 RL J. Immunol. 169:2813-2817(2002).  
 RN [18] PHOSPHORYLATION SITE TYR-393, AND MASS SPECTROMETRY.  
 RP RX PubMed=15592455; DOI=10.1038/nbt1046;  
 RA Rush J., Moritz A., Lee K.A., Guo A., Goss V.L., Spek E.J., Zhang H.,  
 RT "Immunoaaffinity profiling of tyrosine phosphorylation in cancer  
 cells.";

Query Match 100.0%; Score 50; DB 1; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 0.23; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 HYTNASDGL 9
Db	207 HYTNASDGL 215

RESULT 6  
 LCK\_SAISC  
 ID LCK\_SAISC STANDARD; PRT; 508 AA.  
 AC Q95KR7;  
 DT 08-NOV-2005, integrated into UniProtKB/Swiss-Prot.  
 DT 07-MAR-2006, sequence version 2.  
 DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (p56-LCK)  
 DE (Lymphocyte cell-specific protein-tyrosine kinase).  
 GN Name=LCK;  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;  
 OC Cebinae; Saimiri.  
 NCBI\_TaxID=9521;

RN [1] NUCLEOTIDE SEQUENCE [mRNA], ENZYME REGULATION, AND INTERACTION WITH  
 RP SAIMIRINE HERPESVIRUS 2 TIP.  
 RC TISSUE=T-cell;  
 RX MEDLINE=21424508; PubMed=11533187;  
 RX DOI=10.1128/JVI.75.19.9252-9261.2001;  
 RA Greve T., Tamgoune G., Fleischner B., Fickenscher H., Broeker B.M.;  
 RT "Downregulation of p56lck tyrosine kinase activity in T cells of  
 squirrel monkeys (Saimiri sciureus) correlates with the non-  
 transforming and apathogenic properties of herpesvirus saimiri in its  
 natural host.";  
 RT J. Virol. 75:9252-9261(2001).  
 RL  
 CC -!- FUNCTION: Tyrosine kinase that plays an essential role for the  
 selection and maturation of developing T-cell in the thymus and in  
 mature T-cell function. Is constitutively associated with the  
 RT cytoplasmic portions of the CD4 and CD8 surface receptors and  
 plays a key role in T-cell antigen receptor (TCR)-linked signal  
 transduction pathways. Association of the TCR with a peptide  
 antigen-bound MHC complex facilitates the interaction of CD4 and  
 CD8 with MHC class II and class I molecules, respectively, and  
 thereby recruits the associated LCK to the vicinity of the TCR/CD3  
 complex. LCK then phosphorylates tyrosines residues within the

CC immunoreceptor tyrosines-based activation motifs (ITAMS) in the cytoplasmic tails of the TCRgamma chains and CD3 subunits, initiating the TCR/CD3 signaling pathway. In addition, contributes to signaling by other receptor molecules. Associates directly with the cytoplasmic tail of CD2, and upon engagement of the CD2 molecule, LCK undergoes hyperphosphorylation and activation. Also plays a role in the IL2 receptor-linked signaling pathway that controls T-cell proliferative response. Binding of IL2 to its receptor results in increased activity of LCK. Is expressed at all stages of thymocyte development and is required for the regulation of maturation events that are governed by both pre-TCR and mature alpha beta TCR (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein tyrosine phosphate.

CC -!- ENZYME REGULATION: Regulated by phosphatases.

CC -!- SUBUNIT: Binds to the cytoplasmic domain of cell surface receptors, such as CD2, CD4, CD5, CD8, CD44, CD45 and CD122. Also binds to effector molecules, such as PI4K, VAV1, RASA1, FYB and to other proteins kinases including CDC2, RAF1, ZAP70 and SYK. Binds to phosphatidylinositol 3'-kinase (PI3K) from T lymphocytes through its SH3 domain and to the tyrosine phosphorylated form of KDRBS1/p70 through its SH2 domain. Interacts with SQSTM1.

CC -!- Interacts with phosphorylated LIME1. Interacts with CBLB (By similarity). Interacts with sainirine herpesvirus 2 TIP.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic and attached to the membrane. Present in lipid rafts in an unactive form (By similarity).

CC -!- TISSUE SPECIFICITY: Expressed specifically in lymphoid cells.

CC -!- DEVELOPMENTAL STAGE: Levels remain relatively constant throughout T-cell ontogeny.

CC -!- DOMAIN: The SH2 domain mediates interaction with SQSTM1.

CC -!- Interaction is regulated by Ser-58 phosphorylation (By similarity).

CC -!- PTM: Phosphorylated on Tyr-504 presumably by CSK. This phosphorylation downregulates catalytic activity. Phosphorylated on Tyr-393 either by itself or another kinase, leading to increased enzymatic activity.

CC -!- SIMILARITY: Belongs to the Tyr protein kinase family.

CC -!- SIMILARITY: Contains 1 SH2 domain.

CC -!- SIMILARITY: Contains 1 SH3 domain.

CC -!- CAUTION: LCK seems to be active in all vertebrates, except in squirrel monkey T-cells, in which it is inactivated. The reason seems to be that squirrel monkey are the natural host for Saimiriine herpesvirus 2, which is able to efficiently transform T-cells through a mechanism involving viral Tip/ host LCK interaction. Its inactivation may a mechanism that specifically counteracts the transformation effects of viral Tip.

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CC

CC EMBL; AJ277921; CAC38871.1; -; mRNA.

DR HSSP; P06239; 1LKK.

DR SMR; Q95KR7; 64-508.

DR InterPro; IPR00179; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_pk kinase.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR InterPro; IPR001245; Tyr\_pk kinase.

DR InterPro; IPR008266; Tyr\_pk kinase\_AS.

DR Pfam; PF07714; Pkinase\_Tyr; 1.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3\_1; 1.

DR PRINTS; PRO0401; SH2DOMAIN.

DR PRINTS; PRO0452; SH3DOMAIN.

DR PRINTS; PRO0109; TYRKINASE.

DR ProDom; PD000001; Prot\_kinase; 1.

DR ProDom; PD000093; SH2; 1.

DR ProDom; PD000066; SH3; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR SMART; SM00219; TyroKc; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS5001; SH2; 1.

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CC

QY	Match	Score	DB	Length
Query	1 HYTNASDGL 9	50	1	508
Db	207 HYTNASDGL 215	100.0%	1	508
Query Match Best Local Similarity 100.0%; Pred. No. 0.23%; Mismatches 0; Indels 0; Gaps 0;				
Matches 9; Conservative 9;				

RESULT 7

Q7RTZ3\_HUMAN PRELIMINARY; PRT; 509 AA.

ID Q7RTZ3\_HUMAN

AC Q7RTZ3;

DT 15-DEC-2003, integrated into UniProtKB/TREMBL.

DT 07-FEB-2006, entry version 13.

DE Protein tyrosine kinase.

GN Name=LCK;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22289034; PubMed=12401726;

RA Nervi S., Nicodeme S., Gartioux C., Atlan C., Lathrop M., Reviron D., Naquet P., Matsumura F., Imbert J., Vialettes B.;

RT "No association between lck gene polymorphisms and protein level in type 1 diabetes.";

RT Diabetes 51:3326-3330(2002).

RL CC -!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DBJ third party annotation (TPA) entry.

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CC

DR EMBL; BN000073; CAD55807.1; -; Genomic\_DNA.

DR HSSP; P06239; 1BHF.

DR SMR; Q7RTZ3; 65-509.

DR Ensembl; ENSG0000182866; Homo sapiens.

DR GO; GO:0045121; C:lipid raft; ISS.

DR GO; GO:000242; C:pericentriolar material; ISS.

DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.

DR GO; GO:0042169; F:SH2 domain binding; ISS.

RL GO; GO:0006919; P:caspase activation; ISS.

DR GO; GO:003097; P:hemopoiesis; ISS.

DR GO; GO:006917; P:induction of apoptosis; ISS.

DR GO; GO:007242; P:intracellular signaling cascade; ISS.

DR GO; GO:0050870; P:positive regulation of T cell activation; ISS. . . ; ISS.

DR GO; GO:0050862; P:positive regulation of T cell receptor sign. . . ; ISS.

DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

DR GO; GO:0007265; P:Ras protein signal transduction; ISS.

DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.

DR GO; GO:000074; P:regulation of progression through cell cycle; ISS.

DR GO; GO:0030217; P:T cell differentiation; ISS.

DR GO; GO:0006882; P:zinc ion homeostasis; ISS.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_pk kinase.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR InterPro; IPR001245; Tyr\_pk kinase.

DR InterPro; IPR008266; Tyr\_pk kinase\_AS.

DR Pfam; PF07714; Pkinase\_Tyr; 1.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3\_1; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR SMART; PR00109; TYRKINASE.

DR ProDom; PD000001; Prot\_kinase; 1.

DR ProDom; PD000093; SH2; 1.

DR ProDom; PD000066; SH3; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR SMART; SM00219; TyrKC; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

KW Kinase.

SQ SEQUENCE 509 AA; 58001 MW; 44BFF0D43FFB420D CRC64;

Query Match 100.0%; Score 50; DB 2; Length 509;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTNASDGL 9

Db 208 HYTNASDGL 216

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RESULT 8

Q95M32\_9PRIM PRELIMINARY; PRT; 509 AA.

ID Q95M32\_9PRIM PRELIMINARY; PRT; 509 AA.

AC Q95M32; 01-DEC-2001, integrated into UniProtKB/TREMBL.

DT 01-DEC-2001, sequence version 1.

DT 07-FEB-2006, entry version 18.

DE Lck protein.

GN Name=lck;

OS Eukaryota; sp. (gibbon).

OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Hylobatidae; Hylobates.

OX NCBI\_TaxID=9581;

[1] NUCLEOTIDE SEQUENCE.

RX MEDLINE=22031236; PubMed=12033791; DOI=10.1006/viro.2002.1381;

RA Picard C., Greenway A., Holloway G., Olive D., Collette Y.;

RT "Interaction with simian Hck tyrosine kinase reveals convergent evolution of the Nef protein from simian and human immunodeficiency viruses despite differential molecular surface usage.";

RL Virology 295:320-327 (2002). [2]

RN NUCLEOTIDE SEQUENCE.

RA Picard C.;

RL Thesis (2001), Department of Experimental Oncology laboratory, U. CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>.

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CC EMBL; AJ320182; CAC44027.1; -; mRNA.

DR DR HSSP; P06239; ILCK.

DR DR SMR; Q95M32; 65-509.

DR DR GO; GO:0045121; C:lipid raft; ISS.

DR DR GO; GO:0000242; C:pericentriolar material; ISS.

DR DR GO; GO:0004713; F:protein serine/threonine phosphatase activity; ISS.

DR DR GO; GO:0042169; F:SH2 domain binding; ISS.

DR DR GO; GO:0006919; P:caspase activation; ISS.

DR DR GO; GO:003097; P:hemopoiesis; ISS.

DR DR GO; GO:0007242; P:intracellular signaling cascade; ISS.

DR DR GO; GO:0050870; P:positive regulation of T cell activation; ISS. . . ; ISS.

DR DR GO; GO:00050862; P:positive regulation of T cell receptor sign. . . ; ISS.

DR DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.

DR DR GO; GO:0007265; P:Ras protein signal transduction; ISS.

DR DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.

DR DR GO; GO:0000074; P:regulation of progression through cell cycle; ISS.

DR DR GO; GO:0042493; P:response to drug; ISS.

DR DR GO; GO:0030217; P:T cell differentiation; ISS.

DR DR GO; GO:0006882; P:zinc ion homeostasis; ISS.

DR DR InterPro; IPR000719; Prot\_kinase.

DR DR InterPro; IPR002290; Ser\_thr\_pk kinase.

DR DR InterPro; IPR000980; SH2.

DR DR InterPro; IPR001452; SH3.

DR DR InterPro; IPR001245; Tyr\_pk kinase.

DR DR InterPro; IPR008266; Tyr\_pk kinase\_AS.

DR DR Pfam; PF07714; Pkinase\_Tyr; 1.

DR DR Pfam; PF00017; SH2; 1.

DR DR Pfam; PF00018; SH3\_1; 1.

DR DR PRINTS; PR00401; SH2DOMAIN.

DR DR PRINTS; PR00452; SH3DOMAIN.

DR DR SMART; PR00109; TYRKINASE.

DR DR ProDom; PD000001; Prot\_kinase; 1.

DR DR ProDom; PD000093; SH2; 1.

DR DR SMART; SM00252; SH2; 1.

DR DR SMART; SM00326; SH3; 1.

DR DR SMART; SM00219; TyrKC; 1.

DR DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.

DR DR PROSITE; PS50001; SH2; 1.

DR DR PROSITE; PS50002; SH3; 1.

KW Kinase.

SQ SEQUENCE 509 AA; 57947 MW; F1BF5C237C8DB7E CRC64;

Query Match 100.0%; Score 50; DB 2; Length 509;

Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTNASDGL 9

Db 208 HYTNASDGL 216

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RESULT 9

Q73786\_XENLA PRELIMINARY; PRT; 450 AA.

ID Q73786\_XENLA PRELIMINARY; PRT; 450 AA.

AC Q73786; 01-AUG-1998, integrated into UniProtKB/TREMBL.

DT 01-AUG-1998, sequence version 1.

DT 07-FEB-2006, entry version 27.

DE C-Src kinase.

GN Name=CSK; Xenopus laevis (African clawed frog); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

OX NCBI\_TaxID=8355;  
 RN [1] NUCLEOTIDE SEQUENCE.  
 RP Murphy S.M.; Morgan D.O.;  
 RA Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.  
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 CC  
 EMBL; AF052430; AAC05835.1; -; mRNA.  
 HSSP; P41240; 1BYG.  
 SMR; O73786; 4-449.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-Tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00774; Pkinase\_Tyr; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR ProDom; PD00001; Prot\_kinase; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 DR Kinase.  
 KW SEQUENCE 450 AA; 50807 MW; F02FE0557679BA53 CRC64;  
 Query Match 82.0%; Score 41; DB 2; Length 450;  
 Best Local Similarity 77.8%; Pred. No. 15; Mismatches 1; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HYTNASDGL 9  
 Db 155 HYNDADGL 163

RESULT 10

Q81295\_9HEPC PRELIMINARY; PRT; 193 AA.  
 AC Q81295;  
 DT 01-NOV-1996, integrated into UniProtKB/TREMBL.  
 DT 01-FEB-2005, sequence version 3.  
 DT 07-FEB-2006, entry version 23.  
 DE Core protein/E1 protein (Fragment).  
 OS Hepatitis C virus genotype 4.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 RN NCBI\_TaxID=33745;  
 RN [1] NUCLEOTIDE SEQUENCE.  
 RN International consortium for macaque cDNA sequencing and analysis;  
 RT "DNA sequences of macaque genes expressed in brain or testis and its  
 evolutionary implications";  
 RT Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.  
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 CC  
 DR EMBL; AB169165; BAE01257.1; -; mRNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-Tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00017; SH2; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR ProDom; PD00001; Prot\_kinase; 1.  
 DR ProDom; PD00093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.

CC DR EMBL; L36439; AAA45537.1; -; Genomic\_RNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR002521; HCV\_core.  
 DR InterPro; IPR002519; HCV\_env.  
 DR Pfam; PF01542; HCV\_core; 1.  
 DR Pfam; PF01539; HCV\_env; 1.  
 DR Envelope protein; Transmembrane.  
 KW CHAIN <1 65 core protein.  
 FT CHAIN 66 >193 El protein.  
 FT NON\_TER 1 1  
 FT NON\_TER 193 193  
 FT SEQUENCE 193 AA; 20366 MW; 2E167CE47CEC828F CRC64;  
 Query Match 80.0%; Score 40; DB 2; Length 193;  
 Best Local Similarity 87.5%; Pred. No. 9.2;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db QY 1 HYTNASDGL 8  
 Db 67 HYRNASDG 74

RESULT 11

Q4R6L8\_MACFA PRELIMINARY; PRT; 408 AA.  
 ID Q4R6L8\_MACFA PRELIMINARY; PRT; 408 AA.  
 AC Q4R6L8;  
 DT 19-JUL-2005, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 5.  
 DE Testis cDNA, clone: QtSA-17706, similar to human fyn-related kinase (FRK).  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopithecoidea; Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9541;  
 [1] RN  
 RN RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=1594441; DOI=10.1093/molbev/msi187;  
 RA Osada N., Hirata M., Tanuma R., Kubuda J., Hida M., Suzuki Y.,  
 RA Sugano S., Gojobori T., Shen C.-K.J., Wu C.I., Hashimoto K.;  
 RT "Substitution Rate and Structural Divergence of 5'UTR Evolution:  
 RT Comparative Analysis Between Human and Cynomolgus Monkey cDNAs.",  
 RT Mol. Biol. Evol. 22:1976-1982 (2005).  
 RL RN  
 RN RP NUCLEOTIDE SEQUENCE.  
 RG International consortium for macaque cDNA sequencing and analysis;  
 RT "DNA sequences of macaque genes expressed in brain or testis and its  
 evolutionary implications";  
 RT Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.  
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 CC  
 DR EMBL; AB169165; BAE01257.1; -; mRNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-Tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR00719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00017; SH2; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR ProDom; PD00001; Prot\_kinase; 1.  
 DR ProDom; PD00093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.



Qy	1 HYTNASDGL 9	Db	192 HYTKTSDGL 200
RESULT 13			
Q9NTR5_HUMAN			
ID Q9NTR5_HUMAN	PRELIMINARY;	PRT;	505 AA.
AC Q9NTR5;			
DT 01-OCT-2000, integrated into UniProtKB/Trembl.			
DT 04-JAN-2005, sequence version 2.			
DT 07-FEB-2006, entry version 22.			
DE Fyn-related kinase.			
GN Name=FRK; ORFNames=RP11-702N8.1-001;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Cetartiodactyla; Ruminantia; Homo.			
OC NCBI_TaxID=9606;			
RN [1]			
RR NUCLEOTIDE SEQUENCE.			
RA Williams S.; Submitted (MAY-2005) to the EMBL/GenBank/DDJB databases.			
RL [2]			
RN NUCLEOTIDE SEQUENCE.			
RA Lloyd C.; Submitted (MAY-2005) to the EMBL/GenBank/DDJB databases.			
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CC CC Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a> Distributed under the Creative Commons Attribution-NoDerivs License			
DR EMBL; AL121963; CAB87592.2; -; Genomic_DNA.			
DR EMBL; AL357141; CAI16469.1; -; Genomic_DNA.			
DR EMBL; AL121963; CAI16469.1; JOINED; Genomic_DNA.			
DR Ensembl; ENSG0000011816; Homo sapiens.			
DR GO; GO:0005524; F:ATP binding; IEA.			
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR InterPro; IPR000719; Prot_kinase.			
DR InterPro; IPR002290; Ser_thr_pk kinase.			
DR InterPro; IPR000980; SH2.			
DR InterPro; IPR001452; SH3.			
DR InterPro; IPR001245; Tyr_pk kinase.			
DR InterPro; IPR008266; Tyr_pk kinase_AS.			
DR Pfam; PF07714; Pkinase_Tyr; 1.			
DR Pfam; PF00017; SH2; 1.			
DR Pfam; PF00018; SH3_1; 1.			
DR PRINTS; PR00401; SH2DOMAIN.			
DR PRINTS; PR00452; SH3DOMAIN.			
DR PRINTS; PR00109; TYRKINASE.			
DR PRODom; PD000001; Prot_kinase; 1.			
DR PRODom; PD000093; SH2; 1.			
DR PRODom; PD000066; SH3; 1.			
DR SMART; SM00252; SH2; 1.			
DR SMART; SM00326; SH3; 1.			
DR SMART; SM00219; TYRK; 1.			
DR SMART; SM00326; SH3; 1.			
DR PROSITE; PS000107; PROTEIN_KINASE_ATP; 1.			
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.			
DR PROSITE; PS50001; SH2; 1.			
DR PROSITE; PS50002; SH3; 1.			
KW Kinase.			
SQ SEQUENCE 505 AA; 58254 MW; 06EC050DDBCD930B CRC64;			
Query Match 80.0%; Score 40; DB 2; Length 505;			
Best Local Similarity 77.8%; Pred. No. 28;			
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
1 HYTNASDGL 9			
RESULT 14			
Q3ZCM0_BOVIN			
ID Q3ZCM0_BOVIN	PRELIMINARY;	PRT;	509 AA.
AC Q3ZCM0;			
DT 27-SEP-2005, integrated into UniProtKB/Trembl.			
DT 27-SEP-2005, sequence version 1.			
DT 07-MAR-2006, entry version 6.			
DE Hypothetical protein MGCI26900.			
GN Name=MGC126900;			
OS Bos taurus (Bovine).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.			
OC NCBI_TaxID=9913;			
RN [1]			
RP NUCLEOTIDE SEQUENCE.			
RC STRAIN=Crossbred x Angus; TISSUE=Ileum;			
RA Moore S.; Alexander L.; Brownstein M.; Guan L.; Lobo S.; Meng Y.; Tanaguchi M.; Wang Z.; Yu J.; Prange C.; Schreiber K.; Shenmen C.; Wagner L.; Bala M.; Barbazuk S.; Barber S.; Babakaiif R.; Beland J.; Chun E.; Del Rio L.; Gibson S.; Hanson R.; Kirkpatrick R.; Liu J.; Matsuo C.; Mayo M.; Santos R.R.; Stott J.; Tsai M.; Wong D.; Siddiqui A.; Holt R.; Jones S.J.; Marra M.A.; Submitted (AUG-2005) to the EMBL/GenBank/DDJB databases.			
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CC CC Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a> Distributed under the Creative Commons Attribution-NoDerivs License			
DR EMBL; BC102046; AAI02047.1; -; mRNA.			
DR GO; GO:0045121; C:lipid raft; ISS.			
DR GO; GO:0000242; C:pericentriolar material; ISS.			
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; ISS.			
DR GO; GO:0004713; F:protein-tyrosine kinase activity; ISS.			
DR GO; GO:0042169; F:SH2 domain binding; ISS.			
DR GO; GO:0006919; P:caspase activation; ISS.			
DR GO; GO:0030097; P:hemopoiesis; ISS.			
DR GO; GO:0006917; P:induction of apoptosis; ISS.			
DR GO; GO:0007242; P:intracellular signaling cascade; ISS.			
DR GO; GO:0050870; P:positive regulation of T cell activation; ISS.			
DR GO; GO:0050862; P:positive regulation of T cell receptor sign. . . ; ISS.			
DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.			
DR GO; GO:0007265; P:Ras protein signal transduction; ISS.			
DR GO; GO:0051249; P:regulation of lymphocyte activation; ISS.			
DR GO; GO:0000074; P:regulation of progression through cell cycle; ISS.			
DR GO; GO:0042493; P:response to drug; ISS.			
DR GO; GO:0030217; P:T cell differentiation; ISS.			
DR GO; GO:0006882; P:zinc ion homeostasis; ISS.			
DR InterPro; IPR000719; Prot_kinase.			
DR InterPro; IPR002290; Ser_thr_pk kinase.			
DR InterPro; IPR000980; SH2.			
DR InterPro; IPR001452; SH3.			
DR InterPro; IPR001245; Tyr_pk kinase.			
DR InterPro; IPR008266; Tyr_pk kinase_AS.			
DR Pfam; PF07714; Pkinase_Tyr; 1.			
DR Pfam; PF00017; SH2; 1.			
DR Pfam; PF00018; SH3_1; 1.			
DR PRINTS; PR00401; SH2DOMAIN.			
DR PRINTS; PR00452; SH3DOMAIN.			
DR PRODom; PD000066; SH3; 1.			
DR SMART; SM00252; SH2; 1.			
DR SMART; SM00326; SH3; 1.			
DR PROSITE; PS000107; PROTEIN_KINASE_ATP; 1.			
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.			
DR PROSITE; PS50001; SH2; 1.			
KW Kinase.			
SQ SEQUENCE 505 AA; 58254 MW; 06EC050DDBCD930B CRC64;			
Query Match 80.0%; Score 40; DB 2; Length 505;			
Best Local Similarity 77.8%; Pred. No. 28;			
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
1 HYTNASDGL 9			

DR	PROSITE; PS50002; SH3; 1.
KW	Hypothetical protein.
SQ	SEQUENCE 509 AA; 58116 MW; CE0E80DCD6D0F2F8 CRC64;
Query Match	80.0%; Score 40; DB 2; Length 509;
Best Local Similarity	77.8%; Pred. No. 29;
Matches	7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 HYTNASDGL 9         :   208 HYMNRTSDGL 216
RESULT 15	
Q9SH39_ARATH	PRELIMINARY; PRT; 323 AA.
ID	Q9SH39_ARATH
AC	Q9SH39;
DT	01-MAY-2000, integrated into UniProtKB/TREMBL.
DT	07-FEB-2006, entry version 18.
DE	F2K11.9.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.; Submitted (DEC-1999) to the EMBL/GenBank/DDJB databases.
RL	[2]
RN	NUCLEOTIDE SEQUENCE.
RA	Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (DEC-1999) to the EMBL/GenBank/DDJB databases.
RL	[3]
RN	NUCLEOTIDE SEQUENCE.
RA	Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
RL	[4]
RN	NUCLEOTIDE SEQUENCE.
RA	Chewk R., Shinn P., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
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DR	EMBL; AY800609; AAV68845.1; mRNA.
DR	EMBL; AY954768; AAX55094.1; mRNA.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0004550; F:nucleoside diphosphate kinase activity; IEA.
DR	GO; GO:0006241; P:CTP biosynthesis; IEA.
DR	GO; GO:0006183; P:GTP biosynthesis; IEA.
DR	GO; GO:0006228; P:UTP biosynthesis; IEA.
DR	InterPro; IPR02902; DUF26.
DR	InterPro; IPR01564; NDK.
DR	Pfam; PF01657; DUF26; 2.
KW	Hypothetical protein.
SQ	SEQUENCE 324 AA; 35754 MW; A389AA8030E1D89F CRC64;
Query Match	78.0%; Score 39; DB 2; Length 324;
Best Local Similarity	66.7%; Pred. No. 27;
Matches	6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy	1 HYTNASDGL 9         :   Db
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DR	EMBL; AC008047; AAF19714.1; -; Genomic_DNA.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0004550; F:nucleoside diphosphate kinase activity; IEA.
DR	GO; GO:0006241; P:CTP biosynthesis; IEA.
DR	GO; GO:0006183; P:GTP biosynthesis; IEA.
DR	GO; GO:0006228; P:UTP biosynthesis; IEA.
DR	InterPro; IPR02902; DUF26.
DR	InterPro; IPR001564; NDK.
DR	Pfam; PF01657; DUF26; 2.
KW	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Bivalvia; Pelecypoda; Bivalvia; Bivalves; Bivalve Mollusca; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
SQ	SEQUENCE 323 AA; 35717 MW; 1FB68B95F78ECCE4 CRC64;
Query Match	78.0%; Score 39; DB 2; Length 323;
Best Local Similarity	66.7%; Pred. No. 27;
RN	[1]

RA NUCLEOIDE SEQUENCE: L.-J., Faure R.L., Leclerc P.;  
 RA "Bull testicular Haploid Germ Cells Express a Messenger Encoding for a  
 RT Truncated Form of the Protein Tyrosine Kinase HCK.";  
 RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.  
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 -  
 DR EMBL; DQ219802; ABB03777.1; -; mRNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 KW Kinase.  
 SQ SEQUENCE 276 AA; 31529 MW; A3CBD992B78E2CBB CRC64;

Query	Match	Score	DB	Length
Qy 1 HYTNASDGL 9	76.0%	38	2	276
Best Local Matches 7; Similarity 77.8%; Conservative 0; Mismatches 2;	Pred. No. 37; Indels 2; Gaps 0;			
Db 122 HYKKASDGL 130				

RESULT 18  
 Q8AWF1\_BRARE PRELIMINARY; PRT; 525 AA.  
 ID Q8AWF1\_BRARE  
 AC Q8AWF1;  
 DT 01-MAR-2003, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, entry version 16.  
 DE Yes-relayed kinase.  
 GN Name=yrk;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 RN [1] NCBI\_TaxID=7955;  
 RN NUCLEOTIDE SEQUENCE.  
 RA Mead R.S., Horsfield J.A., Khan L.B., Postlethwait J.H., Crosier K.E.,  
 RA "Zebrafish Yrk is a SRC-family kinase implicated in embryonic vascular  
 RT development"; RL Genome Res. 0:0-0 (2003).  
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 -  
 DR HSSP; P00523; 2PTK.  
 DR SMR; Q8AWF1; 1-130, 76-525;  
 DR Ensembl; ENSDARG0000004378; Danio rerio.  
 DR ZFIN; ZDB-GENE-030131-9517; yrk.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00714; Pkinase\_Tyr; 1.  
 DR InterPro; IPR0017; SH2; 1.  
 DR Pfam; PF00018; SH3\_1; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODom; PR00001; Prot kinase; 1.

RESULT 19  
 Q7QE10\_ANOGA PRELIMINARY; PRT; 943 AA.  
 ID Q7QE10\_ANOGA  
 AC Q7QE10;  
 DT 15-DEC-2003, integrated into UniProtKB/TREMBL.  
 DT 07-DEC-2004, sequence version 2.  
 DT 07-FEB-2006, entry version 19.  
 DE ENSANGP0000000570 (Fragment).  
 GN ORFNames=ENSANGG0000000517;  
 OS Anopheles gambiae str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;  
 OC Anophelinae; Anopheles.  
 OX NCBI\_TaxID=180454;  
 RN [1] NUCLEOTIDE SEQUENCE.  
 RC The Anopheles gambiae Sequence Committee;  
 RG "Anopheles gambiae re-annotation";  
 RT Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=PEST;  
 RC The Anopheles gambiae Sequence Committee;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 CC prelimary data.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 CC tyrosine phosphate.  
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 CC  
 DR EMBL; AAAB01008848; EA07075.2; -; Genomic\_DNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR002110; ANK.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pk kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001245; Tyr\_pk kinase.  
 DR InterPro; IPR008266; Tyr\_pk kinase\_AS.  
 DR Pfam; PF00017; SH2; 2.  
 DR PRINTS; PR01415; ANKYRIN.  
 DR Pfam; PF00023; Ank; 5.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR PRODom; PR00001; Prot kinase; 1.

DR ProdDom; PD000001; Prot\_kinase; 1.  
 DR ProdDom; PD000093; SH2; 2.  
 DR SMART; SM00248; ANK; 3.  
 DR SMART; SM00252; SH2; 2.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS50297; ANK REP REGION; 1.  
 DR PROSITE; PS50088; ANK REPEAT; 3.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 2.  
 KW ANK repeat; Tyrosine-protein kinase.  
 FT NON\_TER 943 943  
 SQ SEQUENCE 943 AA; 105680 MW; EOFAF3F24FFDA1C CRC64;

Query Match 76.0%; Score 38; DB 2; Length 943;  
 Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 HYTNASDGL 9  
 Db 391 HYTRFSDDGL 399

RESULT 20

Q2PBR5\_9VIRU PRELIMINARY; PRT; 1114 AA.  
 AC Q2PBR5\_9VIRU  
 DT 07-FEB-2006, integrated into UniProtKB/TREMBL.  
 DT 07-FEB-2006, sequence version 1.  
 DT 07-FEB-2006, entry version 1.  
 DE Polyprotein.  
 OS Tellina virus 1.  
 OC Viruses; unclassified viruses.  
 OX NCBI\_TaxID=321302;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Nobiron I., Galloux M., Henry C., Huet J.C.;  
 RT "Genome structure and polypeptides characterization of Tellina virus  
 1."  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DDJB databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Delmas B.; Submitted (MAR-2005) to the EMBL/GenBank/DDJB databases.  
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 CC  
 DR EMBL; AJ920335; CAI74981.1; -; Genomic\_RNA.  
 KW Polyprotein.  
 FT CHAIN 2 451 VP2 protein.  
 FT CHAIN 452 492 pep41 protein.  
 FT CHAIN 493 499 pep7 protein.  
 FT CHAIN 500 512 pep13 protein.  
 FT CHAIN 513 618 X protein.  
 FT CHAIN 619 830 VP4 protein.  
 FT CHAIN 831 1114 VP3 protein.  
 SQ SEQUENCE 1114 AA; 119739 MW; 658BB0EEDF059E42 CRC64;

Query Match 76.0%; Score 38; DB 2; Length 1114;  
 Best Local Similarity 87.5%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYTNASDGL 8  
 Db 72 HYTNASDGL 79

RESULT 21

Q61JB6\_DROME ID Q61JB6\_DROME PRELIMINARY; PRT; 351 AA.  
 AC Q61JB6; DT 05-JUL-2004, integrated into UniProtKB/TREMBL.

DR ProdDom; PD000001; Prot\_kinase; 1.  
 DR ProdDom; PD000093; SH2; 2.  
 DR SMART; SM00248; ANK; 3.  
 DR SMART; SM00252; SH2; 2.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS50297; ANK REP REGION; 1.  
 DR PROSITE; PS50088; ANK REPEAT; 3.  
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50001; SH2; 2.  
 KW ANK repeat; Tyrosine-protein kinase.  
 FT NON\_TER 943 943  
 SQ SEQUENCE 943 AA; 105680 MW; EOFAF3F24FFDA1C CRC64;

Query Match 76.0%; Score 38; DB 2; Length 943;  
 Best Local Similarity 77.8%; Pred. No. 1.5e+02;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 HYTNASDGL 9  
 Db 391 HYTRFSDDGL 399

RESULT 22

Q6W9M4\_PENMA ID Q6W9M4\_PENMA PRELIMINARY; PRT; 358 AA.  
 AC Q6W9M4\_PENMA  
 DT 05-JUL-2004, integrated into UniProtKB/TREMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE G-alpha subunit.  
 GN Name=gasB;  
 OS Penicillium marneffei.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiomycetes; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Zuber S., Hynes M.J., Andrianopoulos A.;  
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDJB databases.  
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 CC  
 DR EMBL; AY301989; AA024336.1; -; Genomic\_DNA.  
 DR HSSP; P04896; IAZS.  
 DR GO; GO:0005525; F:GTP binding; IEA.  
 DR GO; GO:0004871; F:signal transducer activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR02975; Fungi\_GproteinA.  
 DR InterPro; IPR01019; Gprotein\_alpha\_beta.  
 DR InterPro; IPR011025; Gprotein\_alpha\_insert.  
 DR Pfam; PF00503; G-alpha; 1.  
 DR PRINTS; PR00318; GPROTEINA.  
 DR PRINTS; PR01241; GPROTEINAFNG.  
 DR ProdDom; PD000281; Gprotein\_alpha; 1.  
 DR SMART; SM00275; G\_alpha; 1.

SQ SEQUENCE 358 AA; 41206 MW; 060309D95BAFF6C8 CRC64;  
 RX PubMed=16372010; DOI=10.1038/nature04300;  
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,  
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,  
 RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,  
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,  
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,  
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juwadi P.R.,  
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,  
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,  
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
 RA Kuhara S., Ogasawara N., Kikuchi H.;  
 RT "Genome sequencing and analysis of *Aspergillus oryzae*."  
 DT ----  
 DE Small G-protein Gpa2.  
 GN Name=gpa2;  
 OS Paracoccidioides brasiliensis.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Onygenales; mitosporic Onygenales; Paracoccidioides.  
 OX NCBI\_TaxID=121759;  
 RN [1]  
 RP  
 RA Chen D., Borges-Walmsley M.I., Walmsley A.R.;  
 RT "Paracoccidioides brasiliensis GPA2.";  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
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 CC  
 CC EMBL; AY550248; AAT40564.1; -; Genomic\_DNA.  
 DR GO; GO:0005525; F:GTP binding; IEA.  
 DR GO; GO:0004871; F:signal transducer activity; IEA.  
 DR GO; GO:007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR002975; Fungi\_GproteinA.  
 DR InterPro; IPR001019; Gprotein\_alpha\_bd.  
 DR InterPro; IPR011025; Gprotein\_alpha\_insert.  
 DR Pfam; PF00503; G-alpha; 1.  
 DR PRINTS; PR00318; GPROTEINA.  
 DR PRODOM; PD000281; Gprotein\_alpha; 1.  
 DR SMART; SM00275; G\_alpha; 1.  
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 DT 07-MAR-2006, entry version 6.  
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 RA Arroyo J., Berrian M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,  
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,  
 RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Goble A.,  
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 RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,  
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,  
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 RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,  
 RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,  
 RA Penalva M.A., Perteal M., Price C., Pritchard B.L., Quail M.A.,  
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 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,  
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
 RA Takeuchi M., Tekkaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,  
 RA Machida M., Hall N., Barrell B.G., Denning D.W.;  
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
 Aspergillus fumigatus";  
 OX Nature 438:1151-1156(2005).  
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 RP NUCLTOIDE SEQUENCE.  
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RX PubMed=16372010; DOI=10.1038/nature04300;  
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 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,  
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,  
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juwadi P.R.,  
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 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,  
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
 RA Kuhara S., Ogasawara N., Kikuchi H.;  
 RT "Genome sequencing and analysis of *Aspergillus oryzae*."  
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 DR EMBL; AP007151; BAE55758.1; -; Genomic DNA.  
 SQ SEQUENCE 359 AA; 41202 MW; 70BEC45051B2243A CRC64;

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 DT 07-MAR-2006, entry version 6.  
 DE G protein complex alpha subunit (Gα<sub>A</sub>), putative.  
 GN ORFNames=Afu3g12400;  
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 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
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 OX NCBI\_TaxID=5085;  
 RN [1]  
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 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,  
 RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Goble A.,  
 RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,  
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,  
 RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,  
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,  
 RA Kulkarni R., Kumagai T., Lafont A., Latge J.-P., Li W., Lord A.,  
 RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,  
 RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,  
 RA Penalva M.A., Perteal M., Price C., Pritchard B.L., Quail M.A.,  
 RA Rabinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,  
 RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,  
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,  
 RA Takeuchi M., Tekkaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,  
 RA Machida M., Hall N., Barrell B.G., Denning D.W.;  
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
 Aspergillus fumigatus";  
 OX Nature 438:1151-1156(2005).  
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 RP NUCLTOIDE SEQUENCE.  
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 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,  
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,  
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juwadi P.R.,  
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 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,  
 RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
 RA Kuhara S., Ogasawara N., Kikuchi H.;  
 RT "Genome sequencing and analysis of *Aspergillus oryzae*."  
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 DR EMBL; AP007151; BAE55758.1; -; Genomic DNA.  
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Query Match 74.0%; Score 37; DB 2; Length 359;  
 Best Local Similarity 85.7%; Pred. No. 81; Indels 0; Gaps 0;  
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 DT 05-JUL-2005, sequence version 1.  
 DT 07-MAR-2006, entry version 6.  
 DE G protein complex alpha subunit (Gα<sub>A</sub>), putative.  
 GN ORFNames=Afu3g12400;  
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 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
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 RC STRAIN=RIB 40;

RX PubMed=16372010; DOI=10.1038/nature04300;  
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 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,  
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 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juwadi P.R.,  
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 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
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 DR EMBL; AP007151; BAE55758.1; -; Genomic DNA.  
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Query Match 74.0%; Score 37; DB 2; Length 359;  
 Best Local Similarity 85.7%; Pred. No. 81; Indels 0; Gaps 0;  
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 DT 05-JUL-2005, sequence version 1.  
 DT 07-MAR-2006, entry version 6.  
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 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,  
 RA Kuhara S., Ogasawara N., Kikuchi H.;  
 RT "Genome sequencing and analysis of *Aspergillus oryzae*."  
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 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
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 RT "Genome sequencing and analysis of *Aspergillus oryzae*."  
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 DR EMBL; AP007151; BAE55758.1; -; Genomic DNA.  
 SQ SEQUENCE 359 AA; 41202 MW; 70BEC45051B2243A CRC64;

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 DT 05-JUL-2005, sequence version 1.  
 DT 07-MAR-2006, entry version 6.  
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 RN [1]  
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RX PubMed=16372010; DOI=10.1038/nature04300;  
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 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juwadi P.R.,  
 RA Kato M., Kato Y., Kin T., Kokubun A.,

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DR EMBL; AAHF01000002; EAL92343.1; -; Genomic\_DNA.  
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 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.  
 DR GO; GO:0007165; P:Signal transduction; IEA.  
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 DT 23-NOV-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 9.  
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 RX PubMed=14624247; DOI=10.1371/journal.pbio.0000045;  
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 RA Chinwalla A., Clarke L., Clee C., Coghlan A., Coulson A.,  
 RA D'Bustachio P., Fitch D.H.A., Fulton L.A., Fulton R.E.,  
 RA Griffiths-Jones S., Harris T.W., Hillier L.W., Kamath R.,  
 RA Kuwabara P.E., Mardis E.R., Marra M.A., Miner T.L., Minx P.,  
 RA Mullikin J.C., Plumb R.W., Rogers J.E., Sohrmann M.,  
 RA Spieth J., Stajich J.E., Wei C., Willey D., Wilson R.K., Durbin R.,  
 RA Waterston R.H.;  
 RT "The genome sequence of *Caenorhabditis briggsae*: a platform for  
 comparative genomics.";  
 RL PLoS Biol. 1:166-192 (2003).  
 CC EMBL/GenBank/DDJB whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC

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DR EMBL; CAAC01000127; CAE74258.1; -; Genomic\_DNA.  
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 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.  
 DR GO; GO:0007165; P:Signal transduction; IEA.  
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 DR Pfam; PF00503; G-alpha; 1.  
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 Db 330 HYTNATD 336

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 DT 01-NOV-1999, sequence version 1.  
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 RC STRAIN=FGSC4;  
 RA Chang M.H., Jahng K.-Y.;  
 RA Submitted (APR-1999) to the EMBL/GenBank/DDJB databases.  
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DR EMBL; AF142058; AAD34893.1; -; Genomic\_DNA.  
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 DT 26-APR-2005, sequence version 1.  
 DT 07-MAR-2006, entry version 6.  
 DE Hypothetical protein.  
 GN ORFNames=AN3090.2;  
 OS Aspergillus nidulans FGSC A4.  
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 DR PRINTS; PR00318; GPROTEINA.

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 RC STRAIN=FGSC 4;  
 RX PubMed=16372000; DOI=10.1038/nature04341;  
 RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,  
 RA Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,  
 RA Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J.,  
 RA Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C.,  
 RA Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,  
 RA Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,  
 RA Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,  
 RA Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,  
 RA Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,  
 RA Sachs M.S., Osman S.A., Birren B.W.,  
 RT "Sequencing of *Aspergillus nidulans* and comparative analysis with *A. fumigatus* and *A. oryzae*."  
 RL Nature 438:1105-1115 (2005).  
 CC --!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC  
 EMBL; AACD01000051; EAA63661.1; --; Genomic\_DNA.  
 DR GO; GO:0005525; F:GTP binding; IEA.  
 DR GO; GO:0004871; F:signal transducer activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR002975; Fungi\_GproteinA.  
 DR InterPro; IPR001019; Gprotein\_alpha\_bd.  
 DR Pfam; PF00503; G-alpha; 1.  
 DR PRINTS; PR00318; GPROTEINA.  
 DR SMART; SM00275; G\_alpha; 1.  
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 DR 336 HYTNATD 342  
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 DR RESULT 30  
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 DR ID Q4URA6\_XANCB PRELIMINARY; PRT; 405 AA.  
 DR AC Q4URA6;  
 DR DT 05-JUL-2005, integrated into UniProtKB/TREMBL.  
 DR DT 05-JUL-2005, sequence version 1.  
 DR DE 07-FEB-2006, entry version 4.  
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 DR Xanthomonas campestris pv. campestris (strain 8004).  
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 OC Xanthomonadaceae; Xanthomonas.  
 OC NCBI\_TaxID=314565;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX PubMed=15899963; DOI=10.1101/gr.3378705;  
 RA Qian W., Jia Y., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F., Sun Q.,  
 RA Ying G., Tang D.-J., Tang H., Wu W., Hao P., Wang L., Jiang B.-L.,  
 RA Zeng S., Gu W.-Y., Lu G., Rong L., Tian Y., Yao Z., Fu G., Chen B.,  
 RA Fang R., Qiang B., Chen Z., Zhao G.-P., Tang J.-L., He C.;  
 RT "Comparative and functional genomic analyses of the pathogenicity of  
 RT phytopathogen *Xanthomonas campestris* pv. *campestris*.";  
 RL Genome Res. 15:757-767 (2005).  
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 CC  
 EMBL; CP000050; AAY50417.1; --; Genomic\_DNA.  
 DR GO; GO:0005764; C:lysosome; IEA.  
 DR GO; GO:0004348; F:lysosome organization and biogenesis; IEA.  
 DR GO; GO:0007040; P:lysosome; IEA.  
 DR GO; GO:0006665; P:lysophospholipid metabolism; IEA.  
 DR GO; GO:0045493; P:xyilan catabolism; IEA.  
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 DR PANTHER; PTHR1\_1069; Glyco\_hydro\_30; 1.  
 DR Pfam; PF02055; Glyco\_hydro\_30; 1.  
 KW Complete proteome; Xylan\_degradation.  
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 DR 248 HYTDSDG 255  
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 DR GO; GO:0019001; F:guanyl nucleotide binding; IEA.

DR GO; GO:0004871; F:signal transducer activity; IEA.  
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 DR GO; GO:0007165; P:signal transduction; IEA.  
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 DR InterPro; IPR011025; Gprotein\_insert.  
 DR Pfam; PF00503; G-alpha; 1.  
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 DR Query Match 74.0%; Score 37; DB 2; Length 368;  
 DR Best Local Similarity 85.7%; Pred. No. 83;  
 DR Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DR GN Xanthomonas campestris pv. campestris (strain 8004).  
 DR OS Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
 DR OC Xanthomonadaceae; Xanthomonas.  
 DR NCBI\_TaxID=314565;  
 RN [1]  
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 RX PubMed=15899963; DOI=10.1101/gr.3378705;  
 RA Qian W., Jia Y., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F., Sun Q.,  
 RA Ying G., Tang D.-J., Tang H., Wu W., Hao P., Wang L., Jiang B.-L.,  
 RA Zeng S., Gu W.-Y., Lu G., Rong L., Tian Y., Yao Z., Fu G., Chen B.,  
 RA Fang R., Qiang B., Chen Z., Zhao G.-P., Tang J.-L., He C.;  
 RT "Comparative and functional genomic analyses of the pathogenicity of  
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 EMBL; CP000050; AAY50417.1; --; Genomic\_DNA.  
 DR GO; GO:0005764; C:lysosome; IEA.  
 DR GO; GO:0004348; F:lysosome organization and biogenesis; IEA.  
 DR GO; GO:0007040; P:lysosome; IEA.  
 DR GO; GO:0006665; P:lysophospholipid metabolism; IEA.  
 DR GO; GO:0045493; P:xyilan catabolism; IEA.  
 DR InterPro; IPR001139; Glyco\_hydro\_30.  
 DR PANTHER; PTHR1\_1069; Glyco\_hydro\_30; 1.  
 DR Pfam; PF02055; Glyco\_hydro\_30; 1.  
 KW Complete proteome; Xylan\_degradation.  
 SQ SEQUENCE 405 AA; 43309 MW; 3B22DE622C890CA0 CRC64;  
 DR HYTNASDG 8  
 DR 248 HYTDSDG 255  
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 EMBL; AY634289; AAW02895.1; -; Genomic\_DNA.  
 DR GO; GO:0019001; F:guanyl nucleotide binding; IEA.

Search completed: June 29, 2006, 09:29:46  
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